

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 13, 2002, 07:42:36 ; Search time 3214 seconds

(without alignments)
10458.538 Million cell updates/sec

Title: US-09-786-926-2

Perfect score: 1155
Sequence: 1 atgaacgccacaggggaaccc.....ccagcgctgcgagcatctga 1155Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*
1: gb.ba:*
2: gb.htg:*
3: gb.in:*
4: gb.om:*
5: gb.ov:*
6: gb.pa:*
7: gb.ph:*
8: gb.pl:*
9: gb.pr:*
10: gb.ro:*
11: gb.sts:*
12: gb.sy:*
13: gb.un:*
14: gb.vl:*
15: em.ba:*
16: em.fun:*
17: em.hum:*
18: em.in:*
19: em.mu:*
20: em.om:*
21: em.or:*
22: em.ov:*
23: em.pat:*
24: em.ph:*
25: em.pl:*
26: em.ro:*
27: em.sts:*
28: em.un:*
29: em.vl:*
30: em.htg.hum:*
31: em.htg.in:*
32: em.htg.other:*
33: em.htg.mus:*
34: em.htg.pln:*
35: em.htg.rod:*
36: em.htg.mam:*
37: em.htg.vrt:*
38: em.sy:*
39: em.htgo.hum:*
40: em.htgo.mus:*
41: em.htgo.other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1155	100.0	1566	9	HSEBD4	AF000479 Homo sapi
2	1155	100.0	1582	9	BC014970	BC014970 Homo sapi
3	1155	100.0	41174	9	AC011547	AC011547 Homo sapi
4	1105	95.7	203481	30	AC023470	AC023470 Homo sapi
5	1104.8	95.7	1649	6	AR071762	AR071762 Sequence
6	768.8	66.6	1660	10	MM06074	MM06074 Mus muscu
7	765.6	66.3	7088	10	MM0489247	MM0489247 Mus muscu
8	756.8	65.5	278652	2	AC073809	AC073809 Mus muscu
9	752.8	65.2	172489	2	AC128579	AC128579 Rattus no
10	664.4	57.5	52806	2	AC090158	AC090158 Homo sapi
11	278.2	24.1	978	9	AY011720	AY011720 Lemur cat
12	256.8	22.2	7664	9	HSM803501	AL832194 Homo sapi
13	256	22.2	1134	9	AF022139	AF022139 Homo sapi
14	256	22.2	1137	6	AX085542	AX085542 Sequence
15	256	22.2	2327	9	HSEBD3	X83864 H. sapiens E
16	256	22.2	17341	2	AL772202	AL772202 Homo sapi
17	254.4	22.0	1137	6	AR112475	AR112475 Sequence
18	253.2	21.9	977	4	AY011726	AY011726 Artibeus
19	250.4	21.7	1197	6	AX147832	AX147832 Sequence
20	250.4	21.7	1197	6	AX286722	AX286722 Sequence
21	250.4	21.7	1197	6	AX360904	AX360904 Sequence
22	250.4	21.7	1197	6	AX376585	AX376585 Sequence
23	250.4	21.7	1197	9	AB083602	AB083602 Homo sapi
24	250.4	21.7	1197	9	AF317676	AF317676 Homo sapi
25	250.4	21.7	1198	6	AX138796	AX138796 Sequence
26	250.4	21.7	1400	6	AX253448	AX253448 Sequence
27	250.4	21.7	1695	5	AF164114	AF164114 Fugu rubr
28	250.4	21.7	2147	6	AX244600	AX244600 Sequence
29	250.4	21.7	2191	9	BC034703	BC034703 Homo sapi
30	250.4	21.7	2306	9	AF331840	AF331840 Homo sapi
31	250.4	21.7	100680	9	AC011461	AC011461 Homo sapi
32	245.2	21.2	978	4	AY059700	AY059700 Tadaria
33	245.2	21.2	978	10	AY011704	AY011704 Muscardin
34	244.2	21.1	978	10	AY011714	AY011714 Myocastor
35	243.6	21.1	2757	6	AX083645	AX083645 Sequence
36	243	21.0	978	9	AY011718	AY011718 Cynocepha
37	241	20.9	978	4	AY011732	AY011732 Tragalaph
38	240.4	20.8	1143	9	AF022137	AF022137 Homo sapi
39	240.4	20.8	1146	6	AX083646	AX083646 Sequence
40	240.4	20.8	2757	9	HUMEDG	M31210 Human endot
41	239.8	20.8	978	4	AY011694	AY011694 Sorex ara
42	239.6	20.7	978	4	AY011693	AY011693 Condylura
43	239.2	20.6	52806	2	AC090158	AC090158 Homo sapi
44	238.2	20.6	978	4	AY011734	AY011734 Okapia jo
45	237.4	20.6	1149	9	AF233365	AF233365 Homo sapi

ALIGNMENTS

RESULT 1
HSEBD4 1566 bp mRNA linear PRI 17-NOV-1998
LOCUS Homo sapiens mRNA for putative G-protein coupled receptor, ED66.
DEFINITION
ACCESSION AF000479.1 GI:3805931
VERSION
KEYWORDS edg6 gene; G-protein coupled receptor.
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1566)
AUTHORS Graeler M.H.
TITLE Direct Submission
JOURNAL Submitted (16-JUL-1997) Graeler M.H., Molekulare Tumorgenetik,

Max-Debrueck-Centrum, Robert-Rössle-Strasse 10, 13122 Berlin,
GERMANY
2 (bases 1 to 1566)
REFERENCE
AUTHORS
TITLE
ED66, a novel G-protein-coupled receptor related to receptors for
bioactive lysophospholipids, is specifically expressed in lymphoid
tissue
JOURNAL
MEDLINE
PUBMED
Genomics 53 (2), 164-169 (1998)
99009331
9790765

FEATURES

Location/Qualifiers

1..1566
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_type="dendritic cells"
/note="In vitro differentiated from blood cells with IL-4
and GM-CSF"
gene
23..1177
/gene="edg6"
23..1177
/gene="edg6"
/codon_start=1
/product="putative G-Protein coupled receptor, EDG6"
/protein_id="CA04118.1"
/db_xref="GI:3805932"
/translation="MNATGTPVAPESCCOQLAAGSHRLVLYHNHSGRLAGRGEDG
GLGALRGLSVASCLVLENLVLAITSNHRSSRWYVYCLVNLITSLDITGAAYLAN
VLGSLGRTFRLPAQWLEFLEGLFTALASTFSLFTAGRFATWVRYPAEAGATKTS
RVYGFGLCWLALILGMLPLGNMCLAFPRCSLPLVLSKRYILFCLVIFAGLAT
IMGLYGFRLVQASQKAPRPAARRKRLKLYLILVLAFLVGLADVF
GSNLAQOEYLRGMWILALAVLSAVNFIYSPFSRVCAVLSFCCCLRLGRGP
GDCIARVNAHSGASTDSLRPRDSFGRSRLSFRMRPLSSISSVRS1"

*sig_peptide

BASE COUNT 211 a 536 c 523 g 296 t
ORIGIN

Query Match 100.0%; Score 1155; DB 9; Length 1566;
Best Local Similarity 100.0%; Pred. No. 2.4e-140;
Matches 1155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAAGCCACGGGAGACCCGCTGGCCCGAGTCTCTGCCAACAGCTGGCGCGGCG 60
DB 23 ATGAAGCCACGGGAGACCCGCTGGCCCGAGTCTCTGCCAACAGCTGGCGCGGCG 82
QY 61 CACAGCGGCTCATTTGTTCTGACACACACACACACACACACACACACACACAC 120
DB 83 CACAGCGGCTCATTTGTTCTGACACACACACACACACACACACACACACACAC 142
QY 121 CCGAGAGATGCGGCTTGGGAGCCCTGCGGGGCTGTGCTGCGTGGCCGACACTGCTG 180
DB 143 CCGAGAGATGCGGCTTGGGAGCCCTGCGGGGCTGTGCTGCGTGGCCGACACTGCTG 202
QY 181 GTGCTGAGAACATGCTGCTGCTGGCGGCATCACAGCAGACATCGGTGCGGAGCTGG 240
DB 203 GTGCTGAGAACATGCTGCTGCTGGCGGCATCACAGCAGACATCGGTGCGGAGCTGG 262
QY 241 GTCTACTATTGCTGTGATACATCAGCTAGTACCTCTACAGGGGCGGCGCTACTG 300
DB 263 GTCTACTATTGCTGTGATACATCAGCTAGTACCTCTACAGGGGCGGCGCTACTG 322
QY 301 GCCAACGTGCTGTGCGGGGAGCCGACACTTCCGTCGTGGCGCCGCCAAGTGTCTTA 360
DB 323 GCCAACGTGCTGTGCGGGGAGCCGACACTTCCGTCGTGGCGCCGCCAAGTGTCTTA 382
QY 361 CCGGAGGAGGCTGCTCTTACAGCCGCTGCGCGCTCCACCTCAGCGCTGCTTCACATGCA 420
DB 383 CCGGAGGAGGCTGCTCTTACAGCCGCTGCGCGCTCCACCTCAGCGCTGCTTCACATGCA 442
QY 421 GGGAGAGCGCTTTGCGACCATGCTGGCGCGGTGGCGGAGAGCGGGGCGACCAAGACACG 480
DB 443 GGGAGAGCGCTTTGCGACCATGCTGGCGCGGTGGCGGAGAGCGGGGCGACCAAGACACG 502

QY 481 CCGCTCTACCGCTTCAATGCGCTCTCTGCTGGCTGCTGGCCGCGGCTGCTGGGATGCTGCT 540
DB 503 CCGCTCTACCGCTTCAATGCGCTCTCTGCTGGCTGCTGGCCGCGGCTGCTGGGATGCTGCT 562
QY 541 TTGCTGAGCTGAGAACTGCTGCTGCTGGCTTGAACCGCTGCTGCTGCTGCTGCTGCTGCT 600
DB 563 TTGCTGAGCTGAGAACTGCTGCTGCTGGCTTGAACCGCTGCTGCTGCTGCTGCTGCTGCT 622
QY 601 TCCAGGCTGATCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
DB 623 TCCAGGCTGATCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 682
QY 661 GCGCTCTATGAGGCGCATCTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
DB 683 GCGCTCTATGAGGCGCATCTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 742
QY 721 GCGGCTGCTGAGGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
DB 743 GCGGCTGCTGAGGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 802
QY 781 CTGCTGCTGCTGAGGCGCGCATCTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
DB 803 CTGCTGCTGCTGAGGCGCGCATCTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 862
QY 841 TGGGCGCAGAGTACCTGCGGCGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
DB 863 TGGGCGCAGAGTACCTGCGGCGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 922
QY 901 GCGGCTGACCCCATCATCTACTCTTCCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 960
DB 923 GCGGCTGACCCCATCATCTACTCTTCCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 982
QY 961 TTCTCTGCTGCGGAGTCTCTCCGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGG 1020
DB 983 TTCTCTGCTGCGGAGTCTCTCCGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGG 1042
QY 1021 GCGGCTGAGGCTCACTCGGAGCTTCCACACCGGACACTCTCTGAGGCGCAAGGAGGAGG 1080
DB 1043 GCGGCTGAGGCTCACTCGGAGCTTCCACACCGGAGCTCTCTGAGGCGCAAGGAGGAGG 1102
QY 1081 TTTCGGGCTCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
DB 1103 TTTCGGGCTCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1162
QY 1141 GTGCGGAGCATCTGA 1155
DB 1163 GTGCGGAGCATCTGA 1177

RESULT 2
BC014970 1582 bp mRNA linear PRI 04-OCT-2001
LOCUS
DEFINITION Homo sapiens, clone MGC:23096 IMAGE:4849349, mRNA, complete cds.
ACCESSION BC014970.1 GI:15929024
VERSION
KEYWORDS
SOURCE
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (01-OCT-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: <http://mgc.ncl.nih.gov>
COMMENT Contact: MGC help desk
Email: cgaps@remail.nih.gov
Tissue Procurement: Dr. Daniel McVicar, DMS/NCI
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bgsc.bc.ca

Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Susana Chen, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
Leticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
Ness, Pawan Pandoh, Anna-Lisa Prabhu, Parvaneh Saeedi, Jacqueline
Schein, Duane Smalish, Michael Smith, Lorraine Spence, Jeff Stott,
Michael Thorne, Miranda Tsai, Natasha van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAL Plate: 34 Row: a Column: 5
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 4503458.

FEATURES

SOURCE

Location/Qualifiers

CDS

1..1582
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/db_xref="taxon:9606"
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/tissue-type="Blood, natural killer cell"
/clone_1ib="NH_MGC_106"
/lab_host="DH10B-R"
/note="Vector: pOTB7"
26..1180
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/translation="MNAITGVAPESCOQLAAGHSRLYLHNHNSRLAGRGPEP
GLALRGLSVAASCLVLELVLAITSMRSRWYLYLVNITSDLTGAYLAN
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RYVGFICWLLALIGMLPLGWNCCADRCSSSLPLVSKRTLLCLVIFAGVAT
IMGLYAFIRLVAGSGOKAPAPARARLRRLKIVMLILAFVCMGLLLADVF
GSNMAOEYIRGMWMLIAVANSAPVPIISFSPRSRCVAVISFLCGGLRLGMRGP
GDCIARVAEHSASSTTDSIRPDSFRGSRSLSFRRRPLSLISSVRSI"

BASE COUNT 223 a 540 c 523 g 296 t
ORIGIN

Query Match 100.0%; Score 1155; DB 9; Length 1582;

Best Local Similarity 100.0%; Pred. No. 2,4e-140;

Matches 1155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ATGAACGCCACGGGGAACCCGGGTGGCCCCGAGTCTGCCAACAGCTGGCGCGCGG 60
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26 ATGAACGCCACGGGGAACCCGGGTGGCCCCGAGTCTGCCAACAGCTGGCGCGCGG 85
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61 CACAGCGGCTCATGTTGTTGACATACACACCTGGGGCGGCTGGCGCGCGGCGG 120
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86 CACAGCGGCTCATGTTGTTGACATACACACCTGGGGCGGCTGGCGCGCGGCGG 145
|||||
121 CCGGAGATGGCGGCGCTGGGGGCCCTGCGGGGGCTGTGCGTGGCCGCCACAGTGCCTG 180
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146 CCGGAGATGGCGGCGCTGGGGGCCCTGCGGGGGCTGTGCGTGGCCGCCACAGTGCCTG 205
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181 GTGCTGGAGAACTTGTGCTGCTGGCGGCATACACGCAATGCGTGGCGGAGCTGG 240
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206 GTGCTGGAGAACTTGTGCTGCTGGCGGCATACACGCAATGCGTGGCGGAGCTGG 265
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241 GTGTACTATTGGCTGTGTAACATCAGCTGAGAGACTCTCTACAGGGCGCGCTTACCTG 300
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266 GTGTACTATTGGCTGTGTAACATCAGCTGAGAGACTCTCTACAGGGCGCGCTTACCTG 325
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301 GCCAAGTGTGCTGTGCGGGGGCCCGACCTTCGCTGTGCGCGCGCGCCACAGTGTCTTA 360
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326 GCCAAGTGTGCTGTGCGGGGGCCCGACCTTCGCTGTGCGCGCGCGCCACAGTGTCTTA 385
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361 CCGGAGGCGCTGTCTTTCACCGCGCGCGCTCCACCTTCAGCTGCTTCACTGCA 420
|||||
386 CCGGAGGCGCTGTCTTTCACCGCGCGCGCTCCACCTTCAGCTGCTTCACTGCA 445

421 GGGGAGCGCTTTGGCCACCATGTGTGCGGCGGTCGGCGGAGCGGGGCCACCAAGACAGC 480
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446 GGGGAGCGCTTTGGCCACCATGTGTGCGGCGGTCGGCGGAGCGGGGCCACCAAGACAGC 505
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481 CCGGTCTACGGCTTCATCGGCTCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 540
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506 CCGGTCTACGGCTTCATCGGCTCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 565
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541 TTGCTGTGCTGGAATGCTGCTGTGCGCTTTCAGACCCCTGCTCCAGCTTCGCCCCCTAC 600
|||||
566 TTGCTGTGCTGGAATGCTGCTGTGCGCTTTCAGACCCCTGCTCCAGCTTCGCCCCCTAC 625
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601 TCCACAGCGCTACATCTCTTCTGCGTGTGATCTTTCGCGCGGCTGTCGTCGTCGTCG 660
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626 TCCACAGCGCTACATCTCTTCTGCGTGTGATCTTTCGCGCGGCTGTCGTCGTCGTCG 685
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721 GCGGCGCGCGCGCAAGCGCGCGCGCTGTCGTAAGACGCTGTGATGATCTGTCGTCGTC 780
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746 GCGGCGCGCGCGCAAGCGCGCGCGCTGTCGTAAGACGCTGTGATGATCTGTCGTCGTC 805
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781 CTGCTGTGCTGCGGCGCGCTCTGCGGCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 840
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806 CTGCTGTGCTGCGGCGCGCTCTGCGGCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 865
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841 TGGGCGCGCGCGCAAGCGCGCGCGCTGTCGTAAGACGCTGTGATGATCTGTCGTCGTC 900
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866 TGGGCGCGCGCGCAAGCGCGCGCGCTGTCGTAAGACGCTGTGATGATCTGTCGTCGTC 925
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901 GCGGTCAACCCCATCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 960
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926 GCGGTCAACCCCATCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 985
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961 TTCTCTGTCTGCGGCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1020
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986 TTCTCTGTCTGCGGCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1045
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1021 GCGGTCAACCCCATCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1080
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1046 GCGGTCAACCCCATCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1105
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1081 TTTCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1140
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1106 TTTCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1165
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1141 GTGCGGAGCATCTGA 1155
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1166 GTGCGGAGCATCTGA 1180
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RESULT 3
AC011547 41174 bp DNA linear PRI 29-JUN-2000
LOCUS
DEFINITION
AC011547 Homo sapiens chromosome 19 clone LNLN-27205, complete sequence.
AC011547.4 GI:8810260
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 41174)
DOE Joint Genome Institute and Stanford Human Genome Center.
AUTHORS
TITLE
JOURNAL
REFERENCE
2 (bases 1 to 41174)
DOE Joint Genome Institute.
AUTHORS
TITLE
JOURNAL
Submitted (07-OCT-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

REFERENCE 3 (bases 1 to 41174)
 AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
 TITLE Direct Submission
 JOURNAL Submitted (29-JUN-2000) DOE Joint Genome Institute, 2800 Mitchell
 Drive, Walnut Creek, CA 94598, USA
 COMMENT On Jun 29, 2000 this sequence version replaced gi:7711535.
 Draft Sequence Produced by DOE Joint Genome Institute
 www.jgi.doe.gov
 Finishing Completed at Stanford Human Genome Center
 www-shgc.stanford.edu
 Quality: Phrap Quality >=40 99.9% of Sequence;
 Estimated Total Number of Errors is 0.2.
 SFS Content:
 WI-15783 G22974.

FEATURES
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 /db_xref="taxon:9606"
 /chromosome="19"
 /clone="TILNLR-272C5"

BASE COUNT 7477 a 12450 c 11967 g 9280 t

ORIGIN

Query Match 100.0%; Score 1155; DB 9; Length 41174;
 Best Local Similarity 100.0%; Pred. No. 1.1e-140;
 Matches 1155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY - 1 ATGAAGCCACAGGGGAGCCCGGAGTCCCTCCCAACAGCTGGGGCGGGCGG 60
 Db 9925 ATGAAGCCACAGGGGAGCCCGGAGTCCCTCCCAACAGCTGGGGCGGGCGG 9984

QY 61 CACAGCCGGCTATTGTTGCACTACAACACTCGGGCGGGCTGGCGGGGGG 120
 Db 9985 CACAGCCGGCTATTGTTGCACTACAACACTCGGGCGGGCTGGCGGGGGG 10044

QY 121 CCGGAGAGTGGCGGCTGGGGGCGCTGGGGGCTGTGGGTGGCCGACGTGCTG 180
 Db 10045 CCGGAGAGTGGCGGCTGGGGGCGCTGGGGGCTGTGGGTGGCCGACGTGCTG 10104

QY 181 GTGCTGGAGAACTTGCTGGTGGTGGGCAATCACACAGCATGCGGTGGCGAGCTG 240
 Db 10105 GTGCTGGAGAACTTGCTGGTGGTGGGCAATCACACAGCATGCGGTGGCGAGCTG 10164

QY 241 GTCTACTATTGCTGGTGAACATCAAGCTGAGTACCTGCTACGGGGCGGCTACCTG 300
 Db 10165 GTCTACTATTGCTGGTGAACATCAAGCTGAGTACCTGCTACGGGGCGGCTACCTG 10224

QY 301 GCCAAGTGTGCTGCGGGGGCGGCAACCTTCGCTGGGGCGGCGCAAGTGTCTCTA 360
 Db 10225 GCCAAGTGTGCTGCGGGGGCGGCAACCTTCGCTGGGGCGGCGCAAGTGTCTCTA 10284

QY 361 CGGAGGGCGCTGCTTTCACCGCGCTGCGCTTCACCTTCAGCTGCTTCTACATGCA 420
 Db 10285 CGGAGGGCGCTGCTTTCACCGCGCTGCGCTTCACCTTCAGCTGCTTCTACATGCA 10344

QY 421 GGGAGAGGCTTTGCGACATGAGTGGGGCGGCGGAGAGCGGGGCGCACCAAGACGAGC 480
 Db 10345 GGGAGAGGCTTTGCGACATGAGTGGGGCGGCGGAGAGCGGGGCGCACCAAGACGAGC 10404

QY 481 CGCGTACGAGCTTTCATGAGCTGCTGAGCTGAGCGCGGCTGCTGAGGAGTGGCTGCT 540
 Db 10405 CGCGTACGAGCTTTCATGAGCTGCTGAGCTGAGCGCGGCTGCTGAGGAGTGGCTGCT 10464

QY 541 TTGCTGGGCGTGAAGTGGCGCTTTCAGCGCTGCTCAGAGCTTTCAGCGCTTAC 600
 Db 10465 TTGCTGGGCGTGAAGTGGCGCTTTCAGCGCTGCTCAGAGCTTTCAGCGCTTAC 10524

QY 601 TCCAAAGCGCTACATCTCTTCTGCGGTGATCTTCGCGGCGTCTGGCCACCATCATG 660
 Db 10525 TCCAAAGCGCTACATCTCTTCTGCGGTGATCTTCGCGGCGTCTGGCCACCATCATG 10584

QY 661 GGCTCTATGGGGCATCTTCGCGCTGTGCGAGGCGCACGGGCGAAGGCCCGCCAGGCCCA 720
 Db 10585 GGCTCTATGGGGCATCTTCGCGCTGTGCGAGGCGCACGGGCGAAGGCCCGCCAGGCCCA 10644

Db 10585 GGCTCTATGGGGCATCTTCGCGCTGTGCGAGGCGCACGGGCGAAGGCCCGCCAGGCCCA 10644

QY 721 GCGGCCCGCGCAAGGCCCGCGCTGCTGAAGAGCTGCTGATGATCTGCTGGCTTC 780
 Db 10645 GCGGCCCGCGCAAGGCCCGCGCTGCTGAAGAGCTGCTGATGATCTGCTGGCTTC 10704

QY 781 CTGCTGTGCTGGGGCCCATCTTTCGGGCTGCTGCTGCGGACGCTTTTGGCTCCACCTC 840
 Db 10705 CTGCTGTGCTGGGGCCCATCTTTCGGGCTGCTGCTGCGGACGCTTTTGGCTCCACCTC 10764

QY 841 TGGGCCAGAGTACCTGCGGGGCGATGAGCTGATGATCTGCGCTGCGCTCAACTCG 900
 Db 10765 TGGGCCAGAGTACCTGCGGGGCGATGAGCTGATGATCTGCGCTGCGCTCAACTCG 10824

QY 901 GCGGTCAACCCCATCTTACTCTCTCCGAGAGGAGGAGTGTGACAGACCGTGTACG 960
 Db 10825 GCGGTCAACCCCATCTTACTCTCTCCGAGAGGAGGAGTGTGACAGACCGTGTCTACG 10884

QY 961 TTTCCTGCTGGGGGTGCTCCGGCTGGGCGATGCGAGGGGCCGGGACTGCTGCGCCGG 1020
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QY 1021 GCGGTGAGGCTACCTCCGAGGCTTCACACCGACAGCTCTGAGGCCAAGGAGACAGC 1080
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 XX AC023470.2
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 DT 15-FEB-2000 (Rel. 62, Created)
 DT 10-JUL-2000 (Rel. 64, Last updated, Version 5)
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 DE unordered pieces.
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 KW HMG; HTGS_DRAFT; HTGS_PHASE1.
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 OS Homo sapiens (human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
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 RN [1]
 RP 1-203481
 RA Waterston R.H.;
 RT "The sequence of Homo sapiens clone";
 RL unpublished.
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 RN [2]
 RP 1-203481
 RA Waterston R.H.;
 RT ;
 RL Submitted (14-FEB-2000) to the EMBL/Genbank/DBJ databases.
 RL Genome Sequencing Center, Washington University School of Medicine, 4444
 RL Forest Park Parkway, St. Louis, MO 63108, USA
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 CC On Feb 23, 2000 this sequence version replaced gi:6970697.
 CC ----- Genome Center -----
 CC Center: Washington University Genome Sequencing Center
 CC Center code: WUGSC

CC	Web site:	http://genome.wustl.edu/gsc/index.shtml
CC	Project Information	-----
CC	Center project name:	H_NH0554A07
CC	Summary Statistics	-----
CC	Sequencing vector:	M13; 100%
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CC	Chemistry:	Dye-terminator Big Dye; 0% of reads
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CC	Assembly program:	Phrap; version 0.990319
CC	Consensus quality:	185558 bases at least Q40
CC	Consensus quality:	191981 bases at least Q30
CC	Consensus quality:	195164 bases at least Q20
CC	Insert size:	200000; agarose-fp
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CC	Quality coverage:	4.65 in Q20 bases; sum-of-contigs
CC	NOTE:	This is a 'working draft' sequence. It currently consists of 30 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.
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CC	* be preserved.	
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CC	6207	6306: gap of unknown length
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 ORGANISM Mus musculus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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 REFERENCE 1 (bases 1 to 1660)
 AUTHORS Graeler M.H.
 TITLES Direct Submission
 JOURNAL Submitted (11-MAY-1998) Graeler M.H., Molekulare Tumor- und
 Immunogenetik, Max-Delbrueck-Centrum, Robert-Rössle-Str. 10, 13122
 Berlin, GERMANY
 REFERENCE 2 (bases 1 to 1660)

AUTHORS Graeler M.H., Bernhardt G., and Lipp M.
 TITLE EDG6, a novel G-protein-coupled receptor related to receptors for bioactive lysophospholipids, is specifically expressed in lymphoid tissue
 JOURNAL Genomics 53 (2), 164-169 (1998)
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 PUBMED 9790765
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Db 4375 CTGAGCTCTACGAGGCTTCTTAGAGTGGTGGAGCTTGGAGCTTGGAGCTTGGAGCTTGG 4434
OY 718 CCAGCGCGCGCGCGAGAGCGCGCGCTGGTGAAGAGGCTGGTGAATCTTGGCTGGCGC 777
Db 4435 CCGCTGCGCGCGCGAGAACTTCCGAGGCTACTCAACACCGTGTGATGATCTTGGTGGCGC 4494
OY 778 TTTCGTGGTGGCTGGGCGCACTCTTGGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 837
Db 4495 TTTCGTGGTGGCTGGGCGCACTCTTGGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 4554
OY 838 CTCTGGGCGCGAGAGTACCTGGGCGATGAGTGAATCTTGGCTGGCGCTGGCTGGCTGGC 897
Db 4555 GTCTGGGCGCGAGAGTACCTGGGCGATGAGTGAATCTTGGCTGGCGCTGGCTGGCTGGC 4614
OY 898 TGGGCGGCTCAACCCCATCTACTCTTCCGAGAGAGAGTGGTGGTGGTGGTGGTGGTGGTGG 957
Db 4615 TGGGCGGCTCAACCCCATCTACTCTTCCGAGAGAGAGTGGTGGTGGTGGTGGTGGTGGTGG 4674
OY 958 AGTTTCTCTTGGTGGGCTGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGG 1017
Db 4675 AGTTTCTCTTGGTGGGCTGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGG 4734
OY 1018 CGGGCGGCTGGAGCTCGGAGCTTCCAGCACCGACGAGCTCTTGGAGGCGAAGGAGC 1077
Db 4735 CGGATCACCGAGGCGGCTCGGAGCTACACGACTGACAGCTCCCTGGAGGCGCAGGAGC 4794
OY 1078 AGTTTCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGG 1137
Db 4795 AGTTTCTGGAGCTTGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGG 4854
OY 1138 AGCGTGGAGAGCATCT 1153
Db 4855 AGCGTGGAGAGCATCT 4870

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```

RESULT 8
AC073809
LOCUS
DEFINITION
AC073809 278652 bp DNA linear HTG 29-JUN-2000
Mus musculus clone RP23-56M17, WORKING DRAFT SEQUENCE, 36 unordered
pieces
AC073809
AC073809.1 GI:8610426
HTG, HTGS_PHASE1, HTGS_DRAFT.
VERSION
KEYWORDS
MUS MUSCULUS.
SOURCE
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
REFERENCE
1 (bases 1 to 278652)
DOE Joint Genome Institute.
Sequencing of Mouse
Unpublished
2 (bases 1 to 278652)
DOE Joint Genome Institute.
Direct Submission
Submitted (29-JUN-2000) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
-----
Project Information
Center Project Name: 1758681
Center clone name: RPO1-23_56M17.
-----
Summary Statistics
Consensus quality: 252289 bases at least Q40
Consensus quality: 263895 bases at least Q30
Consensus quality: 266429 bases at least Q20
Estimated insert size: 215000; agarose-1p estimation
Estimated insert size: 275152; sum-of-contigs estimation
Quality coverage: 9.55 in Q20 bases; agarose-1p estimation
Quality coverage: 7.47 in Q20 bases; sum-of-contigs estimation.
NOTE: This is a 'working draft' sequence. It currently
consists of 36 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.
1
1045 1044: contig of 1044 bp in length
1144: gap of unknown length
1145 2389: contig of 1245 bp in length
2390 2489: gap of unknown length
2490 3623: contig of 1134 bp in length
3624 3723: gap of unknown length
3724 4950: contig of 1227 bp in length
4951 5050: gap of unknown length
5051 6358: contig of 1308 bp in length
6359 6458: gap of unknown length
6459 7690: contig of 1232 bp in length
7691 7790: gap of unknown length
7791 9195: contig of 1405 bp in length
9196 9295: gap of unknown length
9296 10450: contig of 1155 bp in length
10451 10551: gap of unknown length
10552 11948: contig of 1398 bp in length
11949 12049: gap of unknown length
12050 13214: contig of 1166 bp in length
13215 13315: gap of unknown length
13316 14472: contig of 1158 bp in length
14473 14572: gap of unknown length
14573 15895: contig of 1323 bp in length
15896 15995: gap of unknown length
15996 17073: contig of 1078 bp in length

```

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* 17074 17173: gap of unknown length
* 17174 18506: contig of 1333 bp in length
* 18507 18606: gap of unknown length
* 18607 20221: contig of 1615 bp in length
* 20222 20321: gap of unknown length
* 20322 21675: contig of 1354 bp in length
* 21676 21775: gap of unknown length
* 21776 23648: contig of 1873 bp in length
* 23649 23748: gap of unknown length
* 23749 23878: contig of 2230 bp in length
* 23879 26078: gap of unknown length
* 26079 28123: contig of 2045 bp in length
* 28124 28223: gap of unknown length
* 28224 30661: contig of 2438 bp in length
* 30662 30761: gap of unknown length
* 30762 33105: contig of 2344 bp in length
* 33106 33305: gap of unknown length
* 33306 37129: contig of 3924 bp in length
* 37130 37229: gap of unknown length
* 37230 40019: contig of 2790 bp in length
* 40020 40119: gap of unknown length
* 40120 44618: contig of 4499 bp in length
* 44619 44718: gap of unknown length
* 44719 50463: contig of 5745 bp in length
* 50464 50563: gap of unknown length
* 50564 58865: contig of 8302 bp in length
* 58866 58965: gap of unknown length
* 58966 73594: contig of 14723 bp in length
* 73595 73795: gap of unknown length
* 73796 86431: contig of 12637 bp in length
* 86432 86531: gap of unknown length
* 86532 97864: contig of 11333 bp in length
* 97865 97964: gap of unknown length
* 97965 119089: contig of 21125 bp in length
* 119090 119189: gap of unknown length
* 119190 137271: contig of 18082 bp in length
* 137272 137372: gap of unknown length
* 137373 137472: gap of 17271 bp in length
* 137473 154742: gap of unknown length
* 154743 177021: contig of 22279 bp in length
* 177022 200830: contig of 23709 bp in length
* 200831 200930: gap of unknown length
* 200931 238314: contig of 37384 bp in length
* 238315 238414: gap of unknown length
* 238415 278652: contig of 40238 bp in length.

```

FEATURES

Location/Qualifiers

BASE COUNT 68127 a 71133 c 70594 g 65253 t 3545 others

Query Match 65.5%: Score 756.8; DB 2: Length 278652;
 Best Local Similarity 80.2%: Pred. No. 1.9e-89;
 Matches 927: Conservative 0; Mismatches 222; Indels 7; Gaps 3;

```

QY 1 ATGAGCCACGAGGAGCCCGGTGGCCCGAGTCTGCAACAGCTGCGGCGGCGG 60
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 184593 ATGAGTACCTGTCACGCTGTGTGACCCAGAGTCTGCAACGCGGCGGCGG 184652

QY 61 CACAGCGGCTCATTTTCTGTGACATACACATCTCGGCGGCGGCGGCGGCGG 120
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 184653 CACAGCGCTCTCTGCTGTGCTACATACACAGCGGCGGCGGCGGCGGCGG 184712

QY 121 CCGGAGGA--TGGCGGCTGGGGGCGCTGCGGGGCGTGTGCGCGGCACTGCTG 177
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 184713 TCTGAGGAGCGAGGAGGAGTGTGAGGGGCGCTGCGGAGCGGAGGTTCTTG 184772

QY 178 GTGCTCTGGAGACATGCTGTGCTGCGGCGGCGGCAACGACGATGCGTGGCAGCC 237
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

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Db 184773 GTGCTCTGGAGACGACGATGCTGTGCGGCGCATCCGATCTACATGCGGTCCGCC 184832
QY 238 TGGGTCTACTATTGCTGTGTGACATACAGCTGAGTACCTGCTACAGGCGGCGCTAC 297
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 184833 TGGGTCTACTACTGCTGTGTGACATACAGCTGAGTACCTGCTACAGGCGGCGCTAC 184892

QY 298 CTGCGCAAGTGTCTGTGCGGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 357
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 184893 GTGCTGTAAGTGTCTGTGCAAGGAGCTGTGATCTTCAGTGTGACGCGGTGACG 184952

QY 358 CTACGAGGAGGCGCTCTCTTACCGCCCTGCGGCGGCGGCGGCGGCGGCGGCGG 417
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 184953 CTGCGGAGGCGGCTCTCTCTTACCGCCCTGCGGCGGCGGCGGCGGCGGCGG 185012

QY 418 GCAGGGGAGGCGGCTTGGACCATGAGTGGCGGCGGCGGCGGCGGCGGCGGCGG 477
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 185013 GCGGCGGAGCGGCTTGGACCATGAGTGGCGGCGGCGGCGGCGGCGGCGGCGG 185069

QY 478 AGCGCGCTTACGCGCTTATGAGGCGCTGCTGAGCGGCGGCGGCGGCGGCGG 537
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 185070 AGCGCGCTTATGAGGCGCTTATGAGGCGCTGCTGAGCGGCGGCGGCGGCGG 185129

QY 538 CATTCTGCGGCGGCGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 597
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 185130 CCGCTCTGCGGCGGCGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 185189

QY 598 TACTCCAGCGCTTACATCTCTTCTGCGCTGAGTCTTGGCGGCGGCGGCGGCGG 657
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Db 185190 TACTCCAGCGCTTACATCTCTTCTGCGCTGAGTCTTGGCGGCGGCGGCGGCGG 185249

QY 658 ATGAGGCGCTTATGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 717
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 185250 CTGAGGCGCTTATGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 185309

QY 718 CCAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 777
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 185310 CCAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 185369

QY 778 TTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 837
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 185370 TTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 185429

QY 838 CTTGTGCGGCGGCGGAGTACCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 897
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 185430 CTTGTGCGGCGGCGGAGTACCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 185488

QY 898 TGGGCGGCTAACCCCATCTACTCTTCCGACGAGGAGGTGTGACAGGCGGCTCTC 957
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 185489 TGGGCGGCTAACCCCATCTACTCTTCCGACGAGGAGGTGTGACAGGCGGCTCTC 185548

QY 958 AGCTTCTGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1017
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 185549 AGCTTCTGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 185608

QY 1078 AGCTTCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1137
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 185669 AGCTTCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 185728

QY 1138 AGGCTGCGGAGCATCT 1153
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 185729 AGGCTGCGGAGCATCT 185744

RESULT 9
AC128579/ 172489 bp DNA linear HTG 19-JUN-2002
LOCUS Rattus norvegicus clone CH230-72A11, *** SEQUENCING IN PROGRESS
DEFINITION ***74 unordered pieces.
ACCESSION AC128579

```

VERSION
KEYWORDS
SOURCE
ORGANISM

AC128579.1 GI:21909352
HTG: HTGS_PHASE1.
Rattus norvegicus.
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE
AUTHORS

1 (bases 1 to 172489)
Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
Alshbrooks,S.L., Amaralunge,H.C., Are,J.R., Ayele,M., Banks,T.,
Barbaria,J., Benton,J., Bimaga,K., Blankenburg,K., Bonnin,D.,
Bouck,J., Bowle,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P.,
Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,
Carroll,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
Chen,G., Chen,R., Chen,Z., Chowdhury,I., Christopoulos,C.,
Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,
Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H.,
Doutswalle,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,
Eamhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M.,
Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P.,
Gibelli,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,
Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,
Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J.,
Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B.,
Homs,F., Howard,S., Huber,U., Huiyk,S., Hume,J., Jackson,L.E.,
Jacobson,B., Jia,Y., Johnson,R., Jolyet,S., Joudah,S.,
Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C.,
Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L.,
Li,J., Li,Z., Licharge,O., Lieu,C., Liu,J., Liu,W., Loulseged,H.,
Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J.,
Maheswari,M., Mapa,P., Martin,R., Martindale,A., Martinez,E.,
Massey,E., Mawhney,E., McLeod,M.P., Meador,M., Mel,G., Metzger,M.,
Miner,G., Miner,Z., Mitchell,T., Mohabhat,K., Morgan,M., Morris,S.,
Moser,M., Neal,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N.,
Nguyen,N., Nickerson,E., Nwokwkw,S., Oguh,M., Okwuonu,G.,
Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L.,
Peterson,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y.,
Rives,M., Rojas,A., Kojunokan,I., Rolfe,M., Ruiz,S., Severy,G.,
Scheffer,S., Scott,G., Shen,H., Shooshitari,N., Sisson,I.,
Sodergren,E., Sonalka,T., Sparks,A., Stanley,H., Stone,H.,
Sulton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H.,
Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N., Thomas,S.,
Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R., Wang,Q.,
Wang,S., Ward-Moore,S., Warren,R., Washington,C., Wellington,S.,
Williams,G., Williamson,A., Wleczky,R., Wooden,S., Worley,K.,
Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
Weinstock,G. and Gibbs,R.

Direct Submission
Unpublished
2 (bases 1 to 172489)
Worley,K.C.
Submitted (19-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA

COMMENT

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: hgsc-help@bcm.tmc.edu

Project Information

Center project name: GYIW

Center clone name: CH230-72A11

Sequencing vector: Plasmid

Chemistry: Dye-terminator Big Dye: 100% of reads

Assembly program: Phrap: version 0.990329

Consensus quality: 105806 bases at least Q40

Consensus quality: 112580 bases at least Q30

Consensus quality: 117088 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length

(see http://www.hgsc.bcm.tmc.edu/docs/genbank/draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 74 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1	1100:	contig of 1100 bp in length
1101	1200:	gap of unknown length
1201	2340:	contig of 1140 bp in length
12341	2440:	gap of unknown length
2441	3487:	contig of 1047 bp in length
3488	3587:	gap of unknown length
3588	4867:	contig of 1280 bp in length
4868	4967:	gap of unknown length
4968	6259:	contig of 1292 bp in length
6260	6359:	gap of unknown length
6360	7362:	contig of 1003 bp in length
7363	7462:	gap of unknown length
7463	8659:	contig of 1197 bp in length
8660	8759:	gap of unknown length
8760	9782:	contig of 1023 bp in length
9783	9882:	gap of unknown length
9883	10910:	contig of 1028 bp in length
10911	11010:	gap of unknown length
11011	12663:	contig of 1653 bp in length
12664	12763:	gap of unknown length
12764	14059:	contig of 1296 bp in length
14060	14159:	gap of unknown length
14160	15547:	contig of 1388 bp in length
15548	15647:	gap of unknown length
15648	17502:	contig of 1855 bp in length
17503	17602:	gap of unknown length
17603	19102:	contig of 1500 bp in length
19103	19202:	gap of unknown length
19203	20719:	contig of 1517 bp in length
20720	20819:	gap of unknown length
20820	22008:	contig of 1189 bp in length
22009	22108:	gap of unknown length
22109	23691:	contig of 1533 bp in length
23692	23791:	gap of unknown length
23792	24942:	contig of 1151 bp in length
24943	25042:	gap of unknown length
25043	26988:	contig of 1946 bp in length
26989	27088:	gap of unknown length
27089	28118:	contig of 1030 bp in length
28119	28218:	gap of unknown length
28219	30012:	contig of 1794 bp in length
30013	30112:	gap of unknown length
30113	32123:	contig of 2011 bp in length
32124	32223:	gap of unknown length
32224	33364:	contig of 1141 bp in length
33365	33464:	gap of unknown length
33465	35833:	contig of 2369 bp in length
35834	35933:	gap of unknown length
35934	38118:	contig of 2185 bp in length
38119	38218:	gap of unknown length
38219	39274:	contig of 1056 bp in length
39275	39374:	gap of unknown length
39375	40749:	contig of 1375 bp in length
40750	40849:	gap of unknown length
40850	42447:	contig of 1598 bp in length
42448	42547:	gap of unknown length
42549	43998:	contig of 1451 bp in length
42548	44098:	gap of unknown length
43999	44098:	gap of unknown length
44099	46005:	contig of 1907 bp in length
46006	46105:	gap of unknown length
46106	47944:	contig of 1839 bp in length
47945	48044:	gap of unknown length
48045	50059:	contig of 2015 bp in length
50060	50159:	gap of unknown length

[illegible]

Db 137592	TGGGTGTACTACATGCTCTCTTGAAACATCACCTTAGGAGCACTGCTACAGAGCCTTGAGCTAC	137533
Qy 298	CTGGCAACGATGCTGATGCTGAGGAGGAGCCGACCTTCCGCTGTGAGCGCCGACAGTGGTTC	357
Db 137532	GTGGTCAACGATGCTGATGCTGAGGAACTCGACCTTCCAGCTGTACCTGTGACATCGGTTTC	137473
Qy 358	CTACGGAGAGGAGCTGCTGCTTACCGCCCTTGCCGCTCCACTTGAAGCCTGCTTTCCTACT	417
Db 137472	CTGCGGAGAGGAGCTGCTGCTTCAATGAGCCCTTGCTGCTCCACTTCAAGTCTCTCTTACACA	137413
Qy 418	GCAGGAGAGCCTTGTGCAACATGATGATCGGAGCCGATGGGCGAAGAGGAGGAGCCACCAAGAC	477
Db 137412	GCCGGCGAGGAGCTTCCGACCAATGATGCG---GATGCTGAAGAGGAGGAGCCACCAAGAC	137356
Qy 478	AGCGGCTGTACAGCTTATCGGCTCTCTGCTGAGCTGCTGAGCGCTGCTGAGGATGCTG	537
Db 137355	AGCCCTGTGTATGCTGCTCATATCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	137296
Qy 538	CGTTGCTGAGGCTGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	597
Db 137295	CCCCTGCTGAGGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	137236
Qy 598	TACTCCAGAGCCTTACATCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	657
Db 137235	TACTCCAGAGGCTTATGAGCTCTTGTGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	137176
Qy 658	ATGAGGCTCTATGAGGAGCACTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	717
Db 137175	CTGAGCCTTATACAGGAGGCACTTATGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	137116
Qy 718	CCACAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	777
Db 137115	CCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	137056
Qy 778	TTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	837
Db 137055	TTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	136996
Qy 838	CTTGGGAGGAGGAGTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	897
Db 136995	GTCGGGAGGAGGAGTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	136936
Qy 898	TGCGGAGTCAACCCATCATCTACTCTTCCGACAGGAGGATGCTGCTGCTGCTGCTGCTGCTG	957
Db 136935	TCACCCATCATCTCTCTCATCTTATCTTCCGACAGGAGGATGCTGCTGCTGCTGCTGCTGCTG	136876
Qy 958	AGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1017
Db 136875	ACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	136816
Qy 1018	CGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1077
Db 136815	CGGATCAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	136756
Qy 1078	AGCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1137
Db 136755	AGTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	136696
Qy 1138	AGGCTGCGGAGCATCT 1153	
Db 136695	AGCATCCGACGAGCCT 136680	
RESULT 10		
AC090158/c		
LOCUS	52806 bp	DNA
DEFINITION	Homo sapiens chromosome 11 clone RP11-397J5 map 11, LOW-PASS	HTG 22-MAR-2001
ACCESSION	AC090158	
VERSION	AC090158.2	GI:13431021
KEYWORDS	HTG; HTGS; PHASEO.	
SOURCE	Homo sapiens.	
ORGANISM	Homo sapiens	

REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 52806)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 11, clone RP11-397J5
Unpublished
2 (bases 1 to 52806)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,S., Barina,N., Bastien,V., Boguski,K.L., Boukagalter,B., Brown,A., Camarata,J., Campiolo,A., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P., DeBretell,P., Dewar,K., Diaz,J.S., Dodge,S., Fairo,S., Ferreira,P., Fitzhugh,N., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L., Grand-Pierre,N., Hages,B., Healdor,A., Horton,L., Hulme,J., Iliev,I., Johnson,R., Jones,C., Karatas,A., Larocque,K., Lamazares,R., Landers,T., Lehoczek,J., Levine,R., Liu,G., Maclean,C., Macdonald,P., Margulis,N., Matthews,C., McCallan,M., McEwan,P., McKernan,K., McPheters,R., Meldrim,J., Menus,L., Mihova,T., Mienga,N., Murphy,T., Naylor,J., Nguyen,C., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C., Retta,R., Riebeck,M., Riley,R., Rise,C., Rogov,P., Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Shubbuck,R., Seaman,S., Severy,P., Sounguez,C., Spencer,B., Stangor-Thomann,N., Stojanovic,N., Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Travers,M., Travis,N., Trifillo,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (17-FEB-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
On Mar 22, 2001 this sequence version replaced gi:12957787.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: <http://www.seq.wi.mit.edu>
Contact: sequence.submissions@genome.wi.mit.edu
Project Information
Center project name: 111814
Center Clone name: 397_J5

NOTE: This record contains 66 individual
sequencing reads that have not been assembled into
contigs. Runs of N are used to separate the reads
and the order in which they appear is completely
arbitrary. Low-pass sequence sampling is useful for
identifying clones that may be gene-rich and allows
overlap relationships among clones to be deduced.
However, it should not be assumed that this clone
will be sequenced to completion. In the event that
the record is updated, the accession number will
be preserved.

682: contig of 682 bp in length
1
683 782: gap of 100 bp
783 1475: contig of 693 bp in length
1476 1575: gap of 100 bp
1576 2276: contig of 701 bp in length
2277 2376: gap of 100 bp
2377 3078: contig of 702 bp in length
3079 3178: gap of 100 bp
3179 3881: contig of 703 bp in length
3882 3981: gap of 100 bp
3982 4706: contig of 725 bp in length
4707 4806: gap of 100 bp
4807 5499: contig of 693 bp in length
5500 5599: gap of 100 bp
5600 6314: contig of 715 bp in length
6315 6414: gap of 100 bp
6415 7124: contig of 710 bp in length
7125 7224: gap of 100 bp

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BASE COUNT 170 a 339 c 267 g 202 t

Query Match 24.1%; Score 278.2; DB 9; Length 978;
 Best Local Similarity 60.4%; Pred. No. 4.8e-27;
 Matches 526; Conservative 0; Mismatches 318; Indels 27; Gaps 3;

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 2 AGGAGAAAGGCTGACACCCAGCTGGTGTTCATCCATCTGCTGCTATCATCTCC 61
 185 TGGAGAACTTGTGCTGGCGGCTACACAGCCATAGCGGTGCGAGCGTGGTCT 244
 62 TGGAGAACATCTTGTGTGTGACCATGGAGAACCAAGAGTTCCACCGCCCATGT 121
 245 ACTATTGCTGTGTAACATACGCTAGTACCTGCTGCACAGGGGCGGCGCTACTGGCCA 304
 122 ACTATTTCATGCGAACCTGGCGCTGTCGACCTGTTGGCGGGGCTGCTACATGCGCA 181
 305 ACGATGCTGCTGGGGGCGGCGGCTGCTGGCGGCGGCGGCGGCGGCTGCTAGCGG 364
 182 ACGTCTGCTTTCGGGGGCGGCGGCTGCTGACAGCTACACCGGCGGCGGCTGCTGGGG 241
 365 AGGCGCTGCTGCTGACCGCGCTGGCGGCTGCTGACCTGCTGCTGCTGCTGCTGCTGCT 424
 242 AAGGAGCATGTGCTGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 301
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 302 AGCGTACATACCATGCTGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATG 358
 485 TCTATGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 544
 359 CCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 418
 545 TGGGCTGAGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 604
 419 TGGGCTGAGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 478
 605 AGCGTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 664
 479 AGCATATATCTCTTCTGCAACAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 538
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 539 TCTATGCAAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 598
 735 CCGCGCGCAAGGCGCGCGC-----CTGCTGAGAGCGTGTGA 763
 539 CGCTTCCAAAGGCGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 658
 764 TGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 823
 659 TCGTCTGAGCGCTTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 718
 824 TCTTTGGCTGCAACCTTGGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 883
 719 ---TGGGCGGCAAGGCTGAGAGCTGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 775
 884 TGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 943
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 944 GCAAGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 974
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RESULT 12

HSN803501
 LOCUS HSN803501 7664 bp mRNA linear PRI 10-JUN-2002
 DEFINITION Homo sapiens mRNA; cDNA DKFP686C042 (from clone DKFP686C042).
 ACCESSION AL832194
 VERSION AL832194.1 GI:21732739
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
 1 (bases 1 to 7664)
 Wamut, R., Heuber, D., Mewes, H.W., Well, B., Amid, C. and Wiemann, S.
 Direct Submission
 Submitted (09-JUN-2002) 1, D-85764 Neuherberg, GERMANY
 Cloned from S. Wiemann, Molecular Genome Analysis, German Cancer
 Research Center (DKFZ); Email: s.wiemann@dkfz-heidelberg.de;
 sequenced by AGOMA (Berlin/Germany) within the cDNA sequencing
 consortium of the German Genome Project.
 This clone (DKFP686C042) is available at the RZPD in Berlin.
 Please contact the RZPD: Ressourcenzentrum, Heuberweg 6, 14059
 Berlin-Charlottenburg, GERMANY; Email: clone@rzd.de. Further
 information about the clone and the sequencing project is available
 at <http://mips.gsf.de/proj/cDNA/>.

FEATURES

Location/Qualifiers
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 /db_xref="taxon:9606"
 /clone="DKFP686C042"
 /tissue_type="cDNA-collection"
 /clone_id="686 (synonym: hicc3). Vector pSport1_Sfi; host
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 /dev_stage="adult"

polyA_signal
 polyA_site
 7566..7573

BASE COUNT 2020 a 1872 c 1874 g 1898 t

Query Match 22.2%; Score 256.8; DB 9; Length 7664;
 Best Local Similarity 55.6%; Pred. No. 1.7e-24;
 Matches 536; Conservative 0; Mismatches 422; Indels 6; Gaps 2;

21 GGTGGCCCCGAGTCTGTGCACAGCTGGCGGCGGCGGCGGCGGCGGCGGCTGCTGCTGCT 80
 3788 GATGGCAACTGCTCTCCCGGACGCTGCCAGCGGCTGGGAGAACAGACCTGCGGGA 3847
 81 GCATTAACACCTAGCGGCGGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 140
 3848 GCATTACCACTAGCTGGGAGGTTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 3907
 141 GGCCCTGCGGCGGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 200
 3908 GCTACCAACGCTGCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3967
 201 GCTGGCGGCAATCAACAGCATGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 260
 3968 TTGATTTGCAATCGAATAAATAATTCAACACCGCATTAATTTTCAATTTGGA 4027
 261 CATACGCTGAGTACTGCTACAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 320
 4028 CTTGGCTCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4087
 321 GGCCGCGACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 380
 4088 CAAAGAACGTTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4147
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 4148 GGCCCTGCGGCGGCTGCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4207
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 4208 GATCAAAATGAGGCTTA---GAGCGCAACAGAGGCGAGCGGCTTCTCTCTGATCGG 4264

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 13, 2002, 05:46:18 ; Search time 319 Seconds

(without alignments)
8153.787 Million cell updates/sec

Title: US-09-786-926-2

Perfect score: 1155
Sequence: 1 atgaacgcacacggggagccccc.....ccagcgtgcgagacatcga 1155

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1155	100.0	1155	21	AAx82789 Human edg6 DNA. H
2	1155	100.0	1155	24	AB145809 Human endothelial
3	1155	100.0	1566	24	AB159511 Human endothelial
4	1155	100.0	1568	22	AAH98657 Human EST-derived
5	1155	100.0	1877	21	AAZ9797 CDNA encoding a G-
6	1155	100.0	2270	20	AAx59366 Human EDG-7 recept
7	1155	100.0	9163	24	AB145808 Human endothelial
8	1151.8	99.7	1176	20	AAx59367 Human EDG-7 recept
9	1139	98.6	1637	20	AAV69761 EDG-1-like G-prote

10	1104.8	95.7	1649	19	AAV68602
11	884.2	77.4	4621	23	ABN05827
12	768.8	66.6	1161	21	AAx82790
13	437.8	37.9	1343	20	AAx59377
14	256	22.2	1137	20	AAx36567
15	256	22.2	1137	22	AAx00258
16	256	22.2	1137	24	AB159508
17	254.4	22.0	1137	21	AAZ22300
18	250.4	21.7	1194	22	AA165825
19	250.4	21.7	1194	22	AA165826
20	250.4	21.7	1197	22	AAH51007
21	250.4	21.7	1197	22	AAE25128
22	250.4	21.7	1197	24	ABK12963
23	250.4	21.7	1197	24	AAx98065
24	250.4	21.7	1197	24	AA169403
25	250.4	21.7	1198	22	AAE87722
26	250.4	21.7	1264	24	AA169392
27	250.4	21.7	1335	24	AAx98124
28	250.4	21.7	1400	22	AAx14597
29	250.4	21.7	1503	21	AAAD0132
30	250.4	21.7	1503	21	AAx46033
31	250.4	21.7	2147	22	AAx15901
32	250.4	21.7	2188	22	AAx94206
33	250.4	21.5	1980	21	AA169391
34	248.8	21.5	1980	21	AAZ61489
35	241.6	20.9	6656	24	ABK51005
36	240.4	20.8	1146	22	AAE74416
37	240.4	20.8	1146	24	ABK51006
38	240.4	20.8	2757	22	AAE74415
39	240.4	20.8	2757	24	AB159506
40	240.4	20.8	2774	12	AAQ14147
41	237.4	20.6	1149	20	AAZ09756
42	237.4	20.6	4063	23	ABK42204
43	234.4	20.3	1137	22	AAE62701
44	234.4	20.3	1825	24	ABD32834
45	230.2	19.9	2232	18	AAV58506

ALIGNMENTS

RESULT 1
ID AAX82789 standard; DNA: 1155 BP.
XX AAX82789;
AC
XX
XX 29-JUN-2000 (first entry)
DT
XX
XX Human edg6 DNA.
DE
XX
XX edg6; human; G-coupled receptor; endothelial differentiation gene;
KW antiinflammatory; immunomodulatory; antimicrobial; antiallergic;
KW cytosolic; gene therapy; inflammation; autoimmune disease; allergy;
KW tumor; leukemia; lymphoma; ss.
XX
XX Homo sapiens.
OS
XX
XX DE19846979-A1.
PN
XX
XX 23-MAR-2000.
PD
XX
XX 13-OCT-1998; 98DE-1046979.
PF
XX
XX 11-SEP-1998; 98DE-1043240.
PR
XX
XX (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
PA
XX
XX Graeler M, Bernhardt G, Lipp M;
PI
XX
XX WPI: 2000-258069/23.
DR
XX
XX P-PSDB; AAM90862.

Nucleotide sequenc
Human Lysoc-1 recep
Murine edg6 DNA.
Rat EDG-7 receptor
Human EDG-3 coding
LPA receptor-relat
Human endothelial
Human EDG3b polyP
Nucleotide sequenc
Nucleotide sequenc
Human nPCy9 codin
Nucleotide sequenc
DNA sequence of hu
Human DNA for pote
Human EDG8 recepto
Human PFI-006 enco
Human EDG-8 recept
Human DNA for pote
Human CDNA encodin
Human orphan G pro
Human G protein co
DNA encoding G-pro
Human full-length
Human EDG-8 recept
DNA encoding a 142
Human EDG1 genomic
Angiogenesis prote
CDNA encoding huma
Angiogenesis prote
Human endothelial
Human edg-1c recep
Human EDG-1c recep
Genomic sequence #
Murine EDG3 CDNA.
Endothelial differ
CDNA encoding p1r

PT New human and murine G-coupled receptor EDG (endothelial
PT differentiation gene) 6, useful for modulating inflammatory and immune
PT reactions and for treatment of allergy or tumors
PS
XX Claim 4: Page 7; 12pp; German.

CC This invention describes novel human and murine G-coupled receptors EDG
CC (endothelial differentiation gene) 6 (I and II). The products of the
CC invention have antiinflammatory, immunomodulatory, antimicrobial,
CC antiallergic and cyostatic activity. (I) and (II) are involved in signal
CC transduction. (I), (II) and their fragments, variants and mutants or
CC binding partners, are used therapeutically to modulate the function of
CC blood and body cells, particularly for inhibition of acute and chronic
CC inflammation and to raise specific antibodies against them. They are used
CC as a source of diagnostic oligonucleotides and for gene therapy.
CC Antibodies against (I) and (II) are useful for diagnosis and optionally
CC when coupled to therapeutic agents, toxins or other antibodies, to
CC modulate immune and inflammatory responses for example immunological
CC defects such as inflammation, infection, autoimmune diseases, allergy,
CC tumors, leukemia and lymphoma. This sequence encodes the human EDG6
CC protein described in the method of the invention.

CC
XX Sequence 1155 BP; 139 A; 414 C; 382 G; 220 T; 0 other:

Query Match 100.0%; Score 1155; DB 21; Length 1155;
Best Local Similarity 100.0%; Pred. No. 6, 8e-185;
Matches 1155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAACGCCACGCGGAGCCCGGTCGAGTCGCGACAGCTGCGCGCGCGCGG 60
Db 1 ATGAACGCCACGCGGAGCCCGGTCGAGTCGCGACAGCTGCGCGCGCGCGG 60
QY 61 CACAGCGGCGCTCATGTTCTGCTACTACACACACTGCGCGCGCGCGCGG 120
Db 61 CACAGCGGCGCTCATGTTCTGCTACTACACACACTGCGCGCGCGCGCGG 120
QY 121 CCGAGAGATGCGGCGCTGCGGCGCGCTGCGGCGCGCGCGCGCGCGG 180
Db 121 CCGAGAGATGCGGCGCTGCGGCGCGCTGCGGCGCGCGCGCGCGCGG 180
QY 181 GTGCTGAGAACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
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QY 361 CGGAGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
Db 361 CGGAGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
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Db 481 CGGAGTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
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QY 601 TCCAGAGCGTATACCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
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Db 661 GGCTCTATGGGCGCATCTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
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Db 721 GCGGCGCGCGGAGAGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
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QY 841 TGGGCGCGAGAGTACCTGCGGAGCATGAGTATGCTGCTGCTGCTGCTGCTGCTG 900
Db 841 TGGGCGCGAGAGTACCTGCGGAGCATGAGTATGCTGCTGCTGCTGCTGCTGCTG 900
QY 901 GGGGTCAACCCATATCTACTCTTCCGAGAGAGAGTGTGACAGCGCTGCTGACG 960
Db 901 GGGGTCAACCCATATCTACTCTTCCGAGAGAGAGTGTGACAGCGCTGCTGACG 960
QY 961 TTCTCTGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020
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Db 1021 GCGGTCAAGGCTCACTGCGGAGCTTCCAGACAGAGAGTGTGACAGCGCTGCTGACG 1080
QY 1081 TTTGCGGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140
Db 1081 TTTGCGGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140
QY 1141 GTGCGAGATCTGA 1155
Db 1141 GTGCGAGATCTGA 1155

RESULT 2
ABLA5809
ID ABLA5809 standard; cdna: 1155 BP.
XX
XX ABLA5809;
AC
XX
XX 26-APR-2002 (first entry)
DE Human endothelial differentiation, G-protein coupled receptor 6 cDNA.
XX
XX Human: endothelial differentiation, G-protein coupled receptor 6;
KW EDG6; haplotype; cancer; angiogenesis; inflammation; chromosome 19p13.3;
KW cytostatic; antiinflammatory; gene therapy; SNP;
KW single nucleotide polymorphism; gene; ss.
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OS Homo sapiens.
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FH key Location/Qualifiers
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FT allele replace(1141,A)
FT /*tag= l

WO200206446-A2.
24-JAN-2002.
17-JUL-2001; 2001WO-US22523.
17-JUL-2000; 2000US-218727P.
(GENEA-) GENAISSANCE PHARM INC.
Kilem SE, Koshi B;
WPI; 2002-171804/22.
P-PSDB; AAM48981.

New genetic variants of endothelial differentiation, G-protein coupled
receptor-6 gene for studying expression, function of the gene and
expressing EDG6 protein for use in screening drugs to treat cancer,
inflammation -
Claim 25; Fig 2; 11pp; English.

The present invention provides the gene, protein and cDNA sequences of
the human endothelial differentiation, G-protein coupled receptor 6
(EDG6). Also identified are single nucleotide polymorphisms (SNPs) found
within the sequences. The sequences can be used in the identification of
the haplotype of an individual, and in the treatment of cancer,
angiogenesis and inflammation. The present sequence is the EDG6 cDNA,
the gene for which is found on chromosome 19p13.3.

Sequence 1155 BP; 139 A; 414 C; 382 G; 220 T; 0 other;

Query Match 100.0%; Score 1155; DB 24; Length 1155;
Best local Similarity 100.0%; Pred. No. 6.8e-185;
Matches 1155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ATGAACGCCACGCGGAGACCCCGGTGCGCTCCCAACAGCTGGCGGCGGCGG 60
DB 1 ATGAACGCCACGCGGAGACCCCGGTGCGCTCCCAACAGCTGGCGGCGGCGG 60
OY 61 CACAGCCGCGCTCATTTGTTCTGCATCAACAACACTGGGCGGCGGCGGCGG 120
DB 61 CACAGCCGCGCTCATTTGTTCTGCATCAACAACACTGGGCGGCGGCGGCGG 120
OY 121 CCGGAGAGATGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 180
DB 121 CCGGAGAGATGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 180
OY 181 GTGCTGAGAACTTCTGCTGTGCGGCGCATCACAGCAGCATGCGTCCGAGCTGG 240
DB 181 GTGCTGAGAACTTCTGCTGTGCGGCGCATCACAGCAGCATGCGTCCGAGCTGG 240
OY 241 GTCTACTATTGCGTGGTGAATCATCAAGCTGAGTGAAGCTGTCACGGGCGGCGTACCTG 300
DB 241 GTCTACTATTGCGTGGTGAATCATCAAGCTGAGTGAAGCTGTCACGGGCGGCGTACCTG 300
OY 301 GCCAAGCTGCTGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 360
DB 301 GCCAAGCTGCTGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 360
OY 361 CCGGAGAGGCGCTGCTTCAACGCGCTGGCGGCGCTCACCTTACGCTCTTCACTGCA 420
DB 361 CCGGAGAGGCGCTGCTTCAACGCGCTGGCGGCGCTCACCTTACGCTCTTCACTGCA 420
OY 421 GGGGAGGCGCTTTGCCACCACTGCTGGCGGCGGCGGCGGCGGCGGCGGCGG 480
DB 421 GGGGAGGCGCTTTGCCACCACTGCTGGCGGCGGCGGCGGCGGCGGCGGCGG 480

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DB 421 GGGGAGGCGCTTTGCCACCACTGCTGGCGGCGGCGGCGGCGGCGGCGGCGG 480
OY 481 CCGCTCACGCGCTTCAATCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
DB 481 CCGCTCACGCGCTTCAATCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
OY 541 TTGCTGGGCTGGAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
DB 541 TTGCTGGGCTGGAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
OY 601 TCCAGAGCTTACATCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
DB 601 TCCAGAGCTTACATCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
OY 661 GGCCTTATGAGGCGCATCTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
DB 661 GGCCTTATGAGGCGCATCTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
OY 721 GCGGCGCGCGCAAGGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
DB 721 GCGGCGCGCGCAAGGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
OY 781 CTGCTGTGCTGGGCGCCACTTTCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
DB 781 CTGCTGTGCTGGGCGCCACTTTCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
OY 841 TGGGCGCGAGATACCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 900
DB 841 TGGGCGCGAGATACCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 900
OY 901 GCGGTACACCCATCATCTACTCTTCCGCGAGCGAGGCTGTGCAAGCCGCTGCTCAAC 960
DB 901 GCGGTACACCCATCATCTACTCTTCCGCGAGCGAGGCTGTGCAAGCCGCTGCTCAAC 960
OY 961 TTCTCTGCTGCGGCGGCTTCCGCGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCGG 1020
DB 961 TTCTCTGCTGCGGCGGCTTCCGCGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCGG 1020
OY 1021 GCGGTGAGGCTCACTCCGAGGCTTCACACCGACAGCTCTGTGAGGCGCAAGGAGCAGC 1080
DB 1021 GCGGTGAGGCTCACTCCGAGGCTTCACACCGACAGCTCTGTGAGGCGCAAGGAGCAGC 1080
OY 1081 TTTGCGGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCT 1140
DB 1081 TTTGCGGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCT 1140
OY 1141 GTGCGGAGCATCTGA 1155
DB 1141 GTGCGGAGCATCTGA 1155

RESULT 3
ABL59511
ID ABL59511 standard; cDNA; 1566 BP.
XX ABL59511;
DE 16-JUL-2002 (first entry)
XX
XX Human endothelial cell differentiation gene EDG6 cDNA SEQ ID NO:11.
XX Human endothelial cell differentiation gene; EDG; Lipid synthesis;
XX tumour; lipid associated gene; lipid metabolism; chromosome 19p13.3;
XX gene; ss.
XX Homo sapiens.
XX
XX OS
XX PN
XX WO200227028-A1.
XX
XX PD
XX 04-Apr-2002.
XX
XX 27-SEP-2001; 2001WO-US30366.
XX

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PR 28-SEP-2000; 2000US-0676052.
XX
XX (ATAI-) ATAIRGIN TECHNOLOGIES INC.
XX
PI Skinner MK, Patton JL, Chaudhary J;
XX WPI; 2002-402054/43.
XX
PT Identifying tumor characteristics in a tissue sample taken from a
PT patient, involves determining the copy number or expression level of
PT genes associated with lipid metabolism, synthesis or action -
XX
XX Example 1; Page 71; 113pp; English.
XX
XX The present invention describes a method for identifying tumour
XX characteristics, comprising measuring a copy number or expression level
XX of at least two genes associated with lipid metabolism, synthesis, or
XX action in cells from a patient tissue sample, and comparing the results
XX with a copy number or expression level of the genes in a normal cell.
XX Also described is an array of nucleic acid polymers immobilised on a
XX solid support, comprising a solid support, at least two different nucleic
XX acid polymers which are each specific for a different gene associated
XX with lipid metabolism, synthesis or action, where each nucleic acid
XX polymer is located at a predetermined position on the solid support, and
XX the array comprises nucleic acid polymers which are specific for less
XX than 100 genes other than the selected genes. The method is useful for
XX determining tumour characteristics in a tissue sample taken from a
XX patient. The present sequence represents a human lipid-associated gene
XX related cDNA sequence, which is used in the exemplification of the
XX present invention.
XX
XX Sequence 1566 BP; 211 A; 536 C; 523 G; 296 T; 0 other;
XX
XX Query Match 100.0%; Score 1155; DB 24; Length 1566;
XX Best Local Similarity 100.0%; Pred. No. 6.8e-185;
XX Matches 1155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 ATGAGCCGACGGGAGACCCCGGTGGCCCGAGTCTGCCACAGCTGGCGCGCGGG 60
DB 23 ATGAGCCGACGGGAGACCCCGGTGGCCCGAGTCTGCCACAGCTGGCGCGCGGG 82
QY 61 CACAGCGCGCTCATGTTGCTGCACATCAACCACTGGGGCGGTGGCCCGCGGGGGG 120
DB 83 CACAGCGCGCTCATGTTGCTGCACATCAACCACTGGGGCGGTGGCCCGCGGGGGG 142
QY 121 CCGGAGAGATGGCGGCTGGGGGCGCTGCGGGGGCTGTCGATGGCCCGCAGTGCCTGTG 180
DB 143 CCGGAGAGATGGCGGCTGGGGGCGCTGCGGGGGCTGTCGATGGCCCGCAGTGCCTGTG 202
QY 181 GTGCTGGAGAACTTGTGCTGGTGGCGGCGCATACCAAGCCATGCGGTGCGAGCGTGG 240
DB 203 GTGCTGGAGAACTTGTGCTGGTGGCGGCGCATACCAAGCCATGCGGTGCGAGCGTGG 262
QY 241 GTGTACATATGCTGGTGGAGCAATCAGGTGAGTGCCTGCTCAAGGGGCGGCGCTACCTG 300
DB 263 GTGTACATATGCTGGTGGAGCAATCAGGTGAGTGCCTGCTCAAGGGGCGGCGCTACCTG 322
QY 301 GCCAAGCTGCTGCTGCGGGGGCGGCGCACTTCCGTCTGGCGCGCGCCAGTGGTCTTA 360
DB 323 GCCAAGCTGCTGCTGCGGGGGCGGCGCACTTCCGTCTGGCGCGCGCCAGTGGTCTTA 382
QY 361 CCGGAGGCGCTGCTTTCACCGCGCTGGCGGCTCCACCTTCAAGCCTGCTTTCACCTGA 420
DB 383 CCGGAGGCGCTGCTTTCACCGCGCTGGCGGCTCCACCTTCAAGCCTGCTTTCACCTGA 442
QY 421 GGGGAGCGCTTGGCGCAATGGTGGGGGCGGTGGCGGAGAGGGGGCGCAAGACACAC 480
DB 443 GGGGAGCGCTTGGCGCAATGGTGGGGGCGGTGGCGGAGAGGGGGCGCAAGACACAC 502
QY 481 CGCGTCTAGCGGCTTCAATCGCGCTTGGCTGCTGCTGGCGCGCGCTGCTGGGATGCTGCT 540
DB 503 CGCGTCTAGCGGCTTCAATCGCGCTTGGCTGCTGCTGGCGCGCGCTGCTGGGATGCTGCT 562

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QY 541 TTGCTGGCGCTGGAAGTGCCTGTGCGCCTTTGACCGCGTGCATGACCTTTCGCCCCCTAC 600
DB 563 TTGCTGGCGCTGGAAGTGCCTGTGCGCCTTTGACCGCGTGCATGACCTTTCGCCCCCTAC 622
QY 601 TCCAAAGCGCTACATCCTTCTTTCGCTGTGATCTTTCGCGGGGCTTCGGCCACCATCATG 660
DB 623 TCCAAAGCGCTACATCCTTCTTTCGCTGTGATCTTTCGCGGGGCTTCGGCCACCATCATG 682
QY 661 GGCCTCTAATGAGGGCCATCTTCGCGCTGTGATCTTTCGCGGGGCTTCGGCCACCATCATG 720
DB 683 GGCCTCTAATGAGGGCCATCTTCGCGCTGTGATCTTTCGCGGGGCTTCGGCCACCATCATG 742
QY 721 GCGGCGCGCGCGCAAGGCGCGCGCTGCTGAAGAGCGTGTGATGATCTTCGCGCGCTTC 780
DB 743 GCGGCGCGCGCGCAAGGCGCGCGCTGCTGAAGAGCGTGTGATGATCTTCGCGCGCTTC 802
QY 781 CTGCTGTGCTGGGGCGCCACTTTCGCGCTGCTGCTGCGCGAGCTTTTGGCTCCAACTTC 840
DB 803 CTGCTGTGCTGGGGCGCCACTTTCGCGCTGCTGCTGCGCGAGCTTTTGGCTCCAACTTC 862
QY 841 TGGGCGCGAGATACCTGCGGGGCGATGAGATGATCTTCGCGCGCTTCCTCAACTCG 900
DB 863 TGGGCGCGAGATACCTGCGGGGCGATGAGATGATCTTCGCGCGCTTCCTCAACTCG 922
QY 901 GCGGTCAACCCCATCATCTTCTTCGCGAGAGAGAGTGTGCAAGACCGCTGCTCAGC 960
DB 923 GCGGTCAACCCCATCATCTTCTTCGCGAGAGAGAGTGTGCAAGACCGCTGCTCAGC 982
QY 961 TTCTCTGCTGGGGGTGCTCCGCTGGGCGATGCGAGGGGCGCGGGAGCTGCTGGCGCG 1020
DB 983 TTCTCTGCTGGGGGTGCTCCGCTGGGCGATGCGAGGGGCGCGGGAGCTGCTGGCGCG 1042
QY 1021 GCGGTCAAGGCTCATCTCGGGAGCTTCCACACCAAGCAAGCTTCGAGGCGCAAGGAGACG 1080
DB 1043 GCGGTCAAGGCTCATCTCGGGAGCTTCCACACCAAGCAAGCTTCGAGGCGCAAGGAGACG 1102
QY 1081 TTTTCGCGGCTCCCGCTCGCTCAGCTTTTCGATGCGGGAGCGCCCTGTCAGCATCTCCAGC 1140
DB 1103 TTTTCGCGGCTCCCGCTCGCTCAGCTTTTCGATGCGGGAGCGCCCTGTCAGCATCTCCAGC 1162
QY 1141 GTGCGGAGCATCTGA 1155
DB 1163 GTGCGGAGCATCTGA 1177

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RESULT 4
AAH98657
ID AAH98657 standard; cDNA; 1568 BP.

XX AAH98657;
XX
XX
XX 12-OCT-2001 (first entry)
XX
XX
DE Human EST-derived coding sequence SEQ ID NO: 514.
XX
XX Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
KW diagnostics; forensic test; gene mapping; genetic disorder;
KW biodiversity; gene therapy; nutrition; ss.
XX
XX Homo sapiens.
XX
XX MO200154477-A2.
XX
XX PD 02-AUG-2001.
XX
XX 25-JAN-2001; 2001WO-USO2687.
XX
XX PF 25-JAN-2000; 2000US-0491404.
XX PR 17-JUL-2000; 2000US-0617746.
XX PR 03-AUG-2000; 2000US-0631451.
XX PR 15-SEP-2000; 2000US-0663870.
XX

PA (HYSE-) HYSQ INC.
 XX Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
 PI Cao Y, Drmanac RA, Zhang J, Werhman T;
 XX WPI: 2001-476164/51.
 DR P-PSDB: AAM23998.
 XX Isolated polypeptide for treatment of diseases, diagnostics, raising
 PT antibodies and research use -
 XX
 PS Claim 1: Page 536-537; 1275pp; English.
 XX
 CC The present invention provides the protein and coding sequences of novel
 CC proteins from a variety of organisms, including human, dog, cat, horse,
 CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
 CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
 CC from the organism of interest. They can be used in diagnostics,
 CC forensics, gene mapping, identification of mutations, to assess
 CC biodiversity and for nutritional purposes. The present sequence is a cDNA
 CC of the invention.
 CC
 XX Sequence 1568 BP; 211 A; 536 C; 525 G; 296 T; 0 other;
 SO
 Query Match 100.0%; Score 1155; DB 22; Length 1568;
 Best Local Similarity 100.0%; Pred. No. 6.8e-185;
 Matches 1155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 683 GGGCTATGAGGACATCTTCGCGTGGTGCAGGGCAGAGGGGACAGAGGCCCCACAGCCCA 742
 QY 721 GGGGCCCGCCGAGAGGCCCGCGCTGCTGAAGACGTGTGATATCTCTGTGCTTC 780
 DB 743 GGGGCCCGCCGAGAGGCCCGCGCTGCTGAAGACGTGTGATATCTCTGTGCTTC 802
 QY 781 CTGCTGTGAGGCGCCACTCTTCGGGGTGTGTCGGCCGACGTCTTGAGCTCCAACTC 840
 DB 803 CTGCTGTGAGGCGCCACTCTTCGGGGTGTGTCGGCCGACGTCTTGAGCTCCAACTC 862
 QY 841 TGGGCCAGAGTACTGTGCGGGGACATGAGTGTGATCTTGCCCTGCGCTCTCAACTCG 900
 DB 863 TGGGCCAGAGTACTGTGCGGGGACATGAGTGTGATCTTGCCCTGCGCTCTCAACTCG 922
 QY 901 GCGGTACACCCATCATCTACTCTTCGCCAGACGAGAGGTGTGACAGCCGTCTCAGC 960
 DB 923 GCGGTACACCCATCATCTACTCTTCGCCAGACGAGAGGTGTGACAGCCGTCTCAGC 982
 QY 961 TTCTCTGTGCGGGTGTGTCGGGGTGTGTCGGGGTGTGTCGGGGTGTGTCGGGGTGTG 1020
 DB 983 TTCTCTGTGCGGGTGTGTCGGGGTGTGTCGGGGTGTGTCGGGGTGTGTCGGGGTGTG 1042
 QY 1021 GCCGTGAGGCTCATCTCCGAGCTTCCACACCGACGCTCTGTGAGGCCAAGGACAGC 1080
 DB 1043 GCCGTGAGGCTCATCTCCGAGCTTCCACACCGACGCTCTGTGAGGCCAAGGACAGC 1102
 QY 1081 TTTCGGGCTCCCGCTGCTGCTGACCTTTGCGAGTGCAGGAGCCCTGTCCAGCATCTCCAGC 1140
 DB 1103 TTTCGGGCTCCCGCTGCTGCTGACCTTTGCGAGTGCAGGAGCCCTGTCCAGCATCTCCAGC 1162
 QY 1141 GTGCGAGCATCTGA 1155
 DB 1163 GTGCGAGCATCTGA 1177

RESULT 5
 AA299797
 ID AA299797 standard; cDNA: 1877 BP.
 AC AA299797;
 XX
 DT 12-JUL-2000 (first entry)
 XX
 DE cDNA encoding a G-protein coupled receptor designated 14275 receptor.
 KW Human: G-protein coupled receptor; GPCR; EDG receptor; 14275 receptor;
 KW signalling pathway; GPCR-mediated disorder; anaemia; neutropenia;
 KW thrombocytopenia; inflammation; ss.
 XX
 OS Homo sapiens.
 XX
 FH key Location/Qualifiers
 FT CDS 284..1438
 FT /*tag= a
 FT /*product= "14275 receptor"
 XX
 WO200014233-A1.
 PD 16-MAR-2000.
 PF 03-SEP-1999; 99WO-US20347.
 XX
 PR 03-SEP-1998; 98US-0146416.
 PR 03-SEP-1999; 99US-0390039.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Glucksmann MA, Hodge MR;
 XX
 DR WPI: 2000-256983/22.
 DR P-PSDB: AAY69500.
 XX

PT New G-protein coupled receptor used in receptor assays as a target for
 PT diagnosis and treatment of receptor-mediated disorders including
 PT anaemia, neutropenia or thrombocytopenia or a disorder involving
 PT inflammation -
 XX
 PS Claim 3; Fig 1A-B; 117pp; English.
 CC
 CC The present sequence encodes a human G-protein coupled receptor (GPCR)
 CC which is related to the EDG receptor family. The protein is designated
 CC the 14275 receptor. The 14275 receptor participates in signalling
 CC pathways. The 14275 polypeptide and polynucleotide are used as reagents
 CC or targets in a receptor assay for treatment and diagnosis of
 CC GPCR-mediated disorders. The disorders include anaemia, neutropenia or
 CC thrombocytopenia or a disorder involving inflammation.
 CC
 XX
 SQ Sequence 1877 BP; 312 A; 624 C; 600 G; 341 T; 0 other;

Query Match 100.0%; Score 1155; DB 21; Length 1877;
 Best Local Similarity 100.0%; Pred. No. 6.8e-185;
 Matches 1155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ATGAAGCCACGAGGAGCCCGGTGGCCGCCAGTCTCTGCAACAGCTGGCGCGCGGG 60
 Db 284 ATGAAGCCACGAGGAGCCCGGTGGCCGCCAGTCTCTGCAACAGCTGGCGCGGG 343
 OY 61 CACAGCCGCTATTGTTCTGCACTACAAACACTGCGCGCGCTGGCGCGCGGGGG 120
 Db 344 CACAGCCGCTATTGTTCTGCACTACAAACACTGCGCGCGCTGGCGCGGGGG 403
 OY 121 CCGGAGGATGGGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 180
 Db 404 CCGGAGGATGGGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 463
 OY 181 GTGCTGAGAACTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 240
 Db 464 GTGCTGAGAACTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 523
 OY 241 GTCTACTATTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 300
 Db 524 GTCTACTATTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 583
 OY 301 GCCAAGTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 360
 Db 584 GCCAAGTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 643
 OY 361 CGGAGGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 420
 Db 644 CGGAGGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 703
 OY 421 GGGGAGGCGCTTGGCACCATGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 480
 Db 704 GGGGAGGCGCTTGGCACCATGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 763
 OY 481 CGCGCTACGGCTTATCGGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 540
 Db 764 CGCGCTACGGCTTATCGGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 823
 OY 541 TTGCTGGGCTGGAACCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 600
 Db 824 TTGCTGGGCTGGAACCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 883
 OY 601 TCGAAGGCTACATCTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 660
 Db 884 TCGAAGGCTACATCTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 943
 OY 661 GGCCCTATGGGGCCATTTTCCGCTGGTGTGTGTGTGTGTGTGTGTGTGTGTGT 720
 Db 944 GGCCCTATGGGGCCATTTTCCGCTGGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1003
 OY 721 GCGGCGCGCGCCAGAGCCCGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 780
 Db 1004 GCGGCGCGCGCCAGAGCCCGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1063

OY 781 CTGGTGTGTGGGGCCACCTTGTGGGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 840
 Db 1064 CTGGTGTGTGGGGCCACCTTGTGGGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 1123
 OY 841 TGGGCCAGGAGTACTGTGGGGCATGTGATCTGTGGCCCGCGCTGTCTCAACTCG 900
 Db 1124 TGGGCCAGGAGTACTGTGGGGCATGTGATCTGTGGCCCGCGCTGTCTCAACTCG 1183
 OY 901 GCGGTCAACCCCATCTACTTCTTCCGACGACGAGGATGTGTGTGTGTGTGTGT 960
 Db 1184 GCGGTCAACCCCATCTACTTCTTCCGACGACGAGGATGTGTGTGTGTGTGTGT 1243
 OY 961 TTCTCTGTCTCGGGGTGTCTCGGCTGGGATGTGTGTGTGTGTGTGTGTGTGTGT 1020
 Db 1244 TTCTCTGTCTCGGGGTGTCTCGGCTGGGATGTGTGTGTGTGTGTGTGTGTGTGT 1303
 OY 1021 GCGGTCAAGGCTACTCTCGGAGCTTCCACGACGACGACTGTGTGTGTGTGTGT 1080
 Db 1304 GCGGTCAAGGCTACTCTCGGAGCTTCCACGACGACGACTGTGTGTGTGTGTGT 1363
 OY 1081 TTTCGGGCTTCCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1140
 Db 1364 TTTCGGGCTTCCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1423
 OY 1141 GTGCGAGCATCTGA 1155
 Db 1424 GTGCGAGCATCTGA 1438

RESULT 6
 AAX59366
 ID AAX59366 standard; cdna; 2270 BP.
 XX
 AC AAX59366;
 XX
 DT 20-SEP-1999 (first entry)
 DE
 DE Human EDG-7 receptor homologue cdna.
 XX
 XX

EDG-7: human; HEDG-7: G protein coupled receptor; asthma;
 adult respiratory distress syndrome; Rheumatoid arthritis;
 cardiac ischaemia; acute pancreatitis; septic shock; psoriasis;
 acute cyclosporin nephrotoxicity; diabetic glomerulopathy;
 lung damage; diagnosis; therapy; drug screening;
 antiinflammatory; ss.
 KW
 KW
 KW
 OS Homo sapiens.

Key Location/Qualifiers
 FH 16..1170
 FT CDS /tag= a
 FT /note= "the coding region is specifically claimed
 in Claim 4(a)"
 FT

MO9935106-A2.
 PD 15-JUL-1999.
 XX
 PF 30-DEC-1998; 98MO-CA01196.
 XX
 PR 30-DEC-1997; 97US-0070184.
 XX
 PA (ALIX) ALIEX BIOPHARMACEUTICALS INC.
 XX
 PI Gupta AK, Munroe DG, Zastawny RJ.
 DR WPI: 1999-419322/35.
 DR P-PSDB: AAY06411.
 XX
 XX

A nucleic acid sequence encoding human EDG-7 receptor, useful for
 treating disorders associated with aberrant expression
 XX
 XX
 PS Claim 4(a); Fig 1A; 72pp; English.

FT	allele	/tag= i	replace(4531,A)
FT	allele	/tag= j	replace(4574,T)
FT	allele	/tag= k	replace(4736,T)
FT	allele	/tag= l	replace(4813,T)
FT	allele	/tag= m	replace(5068,T)
FT	allele	/tag= n	replace(5103,T)
FT	allele	/tag= o	replace(5150,A)
FT	allele	/tag= p	replace(5179,A)
FT	allele	/tag= q	replace(5301,A)
FT	allele	/tag= r	replace(5333,A)
FT	allele	/tag= s	replace(5448,C)
FT	allele	/tag= t	replace(5560,A)
FT	allele	/tag= u	replace(5580,A)
FT	allele	/tag= v	replace(5587,T)
FT	allele	/tag= w	replace(5606,C)
FT	allele	/tag= x	
PN	MO200206446-A2.		
PD	24-JAN-2002.		
XX			
XX	17-JUL-2001; 2001MCO-US22523.		
PE			
XX	17-JUL-2000; 2000OUS-218727P.		
PR			
XX	(GENA-1) GENAISSANCE PHARM INC.		
PA			
XX			
PI	Killem SE, Koshy B;		
XX			
DR	WPI: 2002-171804/22.		
XX	P-PDSB; AAM48981.		
XX			
PT	New genetic variants of endothelial differentiation, G-protein coupled		
PT	receptor-6 gene for studying expression, function of the gene and		
PT	expressing EDG6 protein for use in screening drugs to treat cancer,		
PT	inflammation -		
PS	Claim 20: Fig 1: 111pp; English.		
XX			
XX	The present invention provides the gene, protein and cDNA sequences of		
CC	the human endothelial differentiation, G-protein coupled receptor 6		
CC	(EDG6). Also identified are single nucleotide polymorphisms (SNPs) found		
CC	within the sequences. The sequences can be used in the identification of		
CC	the haplotype of an individual, and in the treatment of cancer,		
CC	angiogenesis and inflammation. The present sequence is the EDG6 gene,		
CC	which is found on chromosome 19p13.3.		
XX			
XX	Sequence 9163 BP; 1730 A; 2757 C; 2622 G; 2054 T; 0 other;		
Query Match	100.0%; Score 1155; DB 24; Length 9163;		
Best Local Similarity	100.0%; Pred. No. 6,8e-185;		
Matches 1155; Conservative	0; Mismatches 0; Indels 0; Gaps		
0;			
07	1 ATGAGCCGACGGGGGACCCCGGGGCCCCCGAGTCTCCGCAACGACGCGGGCGGGG 60		
dbb			
4010	ATGAGCCGACGGGGGACCCCGGGGCCCCCGAGTCTCCGCAACGACGCGGGCGGGG 4069		
07	61 CACAGCCGGGTCATTGTCTGCACACCAACCACTCGGGCCGGCGGGCGCGGGGGG 120		

[illegible]

Db 5150 GTGCGAGACATCTGA 5164

RESULT 8

AAK59367
ID AAK59367 standard; cDNA; 1176 BP.

AAK59367;

20-SEP-1999 (first entry)

Human EDG-7 receptor homologue cDNA.

EDG-7; human; HEDG-7; G protein coupled receptor; asthma;
adult respiratory distress syndrome; rheumatoid arthritis;
cardiac ischemia; acute pancreatitis; septic shock; psoriasis;
acute cyclosporin nephrotoxicity; diabetic glomerulopathy;
lung damage; diagnosis; therapy; drug screening;
antiinflammatory; ss.

Homo sapiens.

Location/Qualifiers

13..1167

/tag= a
/note= "the coding region is specifically claimed
in Claim 4(a)"

WO935106-A2.

15-JUL-1999.

30-DEC-1998; 98WO-CA01196.

30-DEC-1997; 97US-0070184.

(ALIX) ALLELIX BIOPHARMACEUTICALS INC.

Gupta AK, Munroe DG, Zastawny RL;

MP1: 1999-419322/35.

P-PSDB; AA06412.

A nucleic acid sequence encoding human EDG-7 receptor, useful for
treating disorders associated with aberrant expression

Claim 4(b); Fig 1B; 72pp: English.

This nucleotide sequence, the coding region of which is claimed,
codes for a novel human homologue of the EDG-7 receptor, i.e.
HEDG-7 (see AAY06411), a 7-transmembrane G protein coupled receptor.
The sequence comprises the cDNA insert of clone pc3-hedg7 M10,
which was obtained from human Jurkat T-cell cDNA by PCR
amplification (see also AAK59371-72). The sequence is nearly
identical to a hedg-7 sequence (see AAK59366) obtained from BAC
and PAC clones. The hedg-7 gene was mapped to chromosome 19p13.3.
Also claimed are an expression vector comprising a HEDG-7 nucleotide
sequence, a host cell, the isolated and purified HEDG-7 receptor,
and methods of using HEDG-7 receptor to identify potential HEDG-7
ligands and antagonists. The hedg-7 nucleotide sequence can be
used in an assay to detect inflammation or disease associated with
CC abnormal levels of HEDG-7 expression. Detection of aberrant
expression of HEDG-7 can accelerate diagnosis and proper treatment
of abnormal conditions, e.g. adult respiratory distress, asthma,
rheumatoid arthritis, cardiac ischemia, acute pancreatitis, septic
shock, psoriasis, acute cyclosporin nephrotoxicity and early
diabetic glomerulopathy, as well as lung damage following exposure
to cigarette smoke, asbestos or silica.

Sequence 1176 BP; 145 A; 419 C; 387 G; 225 T; 0 other;

Query Match 99.7%; Score 1151.8; DB 20; Length 1176;
Best Local Similarity 99.8%; Pred. No. 2.3e-184;

	Matches 1153; Conservative	0; Mismatches	2; Indels	0; Gaps	0;
QY	1	ATGAACGCCACGGGAGACCCCGGTGGCCGCCAGTCTTGCCAAACACTGAGCGGGCGGG	60		
Db	13	ATGAAGCCACGGGGAGACCCCGGTGGCCGCCAGTCTTGCCAAACACTGAGCGGGCGGG	72		
QY	61	CACAGCCGCTCATTTTCTGCACTACACACACACTGGGGCGGCTGGCGGGCGGGGGGG	120		
Db	73	CACAGCCGCTCATTTTCTGCACTACACACACACTGGGGCGGCTGGCGGGCGGGGGGG	132		
QY	121	CCGAGGATGAGCGGCTGGGGGGCGCTGCGGGGGCTGTCGGTGGCCGCACTGCTGTGT	180		
Db	133	CCGAGGATGAGCGGCTGGGGGGCGCTGCGGGGGCTGTCGGTGGCCGCACTGCTGTGT	192		
QY	181	GTGCTGGAGAACTTGTGTGCTGTGCGGCGCATACACGCAATGCGGTGCGGAGCGTGG	240		
Db	193	GTGCTGGAGAACTTGTGTGCTGTGCGGCGCATACACGCAATGCGGTGCGGAGCGTGG	252		
QY	241	GTCTACTATGGCCCTGGGGAACATCACGCTGAGTACCTGTCACGCGGCGGCTACCTG	300		
Db	253	GTCTACTATGGCCCTGGGGAACATCACGCTGAGTACCTGTCACGCGGCGGCTACCTG	312		
QY	301	GCCAACTGCTGCTGTGTCGGGGGGCCGCACTTCCGTGTGGGCCGCCCACTGTCTTA	360		
Db	313	GCCAACTGCTGCTGTGTCGGGGGGCCGCACTTCCGTGTGGGCCGCCCACTGTCTTA	372		
QY	361	CGGAGGGGCTGCTCTTTCACCGCCCTGCGCCCTCCACCTTCAGCCGCTTCACTGCA	420		
Db	373	CGGAGGGGCTGCTCTTTCACCGCCCTGCGCCCTCCACCTTCACTGCACTGCACTG	432		
QY	421	GGGAGGCGCTTTGGCACCATATGTCGGGCGCGGTCGAGAGCGGGGCCACCAAGACACG	480		
Db	433	GGGAGGCGCTTTGGCACCATATGTCGGGCGCGGTCGAGAGCGGGGCCACCAAGACACG	492		
QY	481	CGGCTTACAGGCTTCAATCGGCTCTGCTGGCTGTGGCGCGGCTGCTGGGGAGTGGCT	540		
Db	493	CGGCTTACAGGCTTCAATCGGCTCTGCTGGCTGTGGCGCGGCTGCTGGGGAGTGGCT	552		
QY	541	TTGCTGGGCTGGAGCTGCTGCTGCTGCTTGGACGCTGCTCAAGCCTTTCGCCCTTAC	600		
Db	553	TTGCTGGGCTGGAGCTGCTGCTGCTGCTTGGACGCTGCTCAAGCCTTTCGCCCTTAC	612		
QY	601	TCCAAGCGCTACATCTCTTCTGCTGCTGATCTTTCGCCGCGCTGCTGGCCACATCATG	660		
Db	613	TCCAAGCGCTACATCTCTTCTGCTGCTGATCTTTCGCCGCGCTGCTGGCCACATCATG	672		
QY	661	GGCTCTATGGGGGCAATCTTCGGCTGCTGAGGCGAGCGGGGCGAAGGGCCCAAGCCCA	720		
Db	673	GGCTCTATGGGGGCAATCTTCGGCTGCTGAGGCGAGCGGGGCGAAGGGCCCAAGCCCA	732		
QY	721	GGGCGCCGCGCAAGGCGCGCGCTGCTGAAGACGCTGATGATCTGCTGGCCCTTC	780		
Db	733	GGGCGCCGCGCAAGGCGCGCGCTGCTGAAGACGCTGATGATCTGCTGGCCCTTC	792		
QY	781	CTGCTGCTGGGGCCCACTCTTCCGGCTGCTGCTGGCCCAAGCTTGTGGTCCAACTCT	840		
Db	793	CTGCTGCTGGGGCCCACTCTTCCGGCTGCTGCTGGCCCAAGCTTGTGGTCCAACTCT	852		
QY	841	TGGGGCCAGGATCTCTGCGGGGCAATGAGCTGATCTGCGCCCTGGCCGCTCAACTCG	900		
Db	853	TGGGGCCAGGATCTCTGCGGGGCAATGAGCTGATCTGCGCCCTGGCCGCTCAACTCG	912		
QY	901	GGGATCAACCCCATCATCTACTCTTCGCGACGACGAGAGGTGTGCAGAGCGGTGTCA	960		
Db	913	GGGATCAACCCCATCATCTACTCTTCGCGACGACGAGAGGTGTGCAGAGCGGTGTCA	972		
QY	961	TTCTCTGTGTGGGGTGTCTCGGCTGGGCAATGAGAGGCCCGGGGATGTGCTGGCCGG	1020		
Db	973	TTCTCTGTGTGGGGTGTCTCGGCTGGGCAATGAGAGGCCCGGGGATGTGCTGGCCGG	1032		
QY	1021	GGCGTGGAGCTTCACTCCGAGACTTCCACACGACGACAGCTCTTGAAGGCCAAGGACAGC	1080		
Db	1033	GGCGTGGAGCTTCACTCCGAGACTTCCACACGACGACAGCTCTTGAAGGCCAAGGACAGC	1092		

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QY 1081 TTTCGGGCGTCCGCTCGCTGACATCGGAGAGCCCTGTCAGCATCTCCAGC 1140
    |||
DB 1093 TTTCGGGCGTCCGCTCGCTGACATCGGAGAGCCCTGTCAGCATCTCCAGC 1152
    |||
QY 1141 GTGCGGAGCATCTCGA 1155
    |||
DB 1153 GTGCGGAGCATCTCGA 1167
    |||

RESULT 9
AAV69761
ID AAV69761 standard; cDNA; 1637 BP.
AC AAV69761;
XX
XX 22-FEB-1999 (first entry)
XX
DE EDG-1-like G-protein coupled receptor encoding cDNA.
XX
KM EBV-induced G-protein coupled receptor; EBV-2; Epstein-Barr Virus; ulcer;
KM endohepeliun-differentiation gene; EDG-1-like G-protein coupled receptor;
KM recombinant; agonist; asthma; Parkinson's disease; heart failure; asthma;
KM hypotension; urinary retention; osteoporosis; antagonist; hypertension;
KM angina pectoris; myocardial infarction; allergy; psychosis; depression;
KM migraine; vomiting; stroke; eating disorder;migraine headache; cancer;
KM prostatic hypertrophy; detection; drug screening; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 2..832
    /tag=a
    /transl_except= (pos:620..622; aa:asn)
    /transl_except= (pos:653..655; aa:arg)
    /transl_except= (pos:659..661; aa:thr)
    /product="Edg-1-like G-protein coupled receptor"
FT sig_peptide 2..49
    /tag=b
    /tag=50..829
    /tag=cd
FT mat_peptide 50..829
    /tag=cd
FT
FT
XX W09850549-A2.
XX
XX 12-NOV-1998.
XX
XX 07-MAY-1998; 98WO-US09048.
XX
XX 07-MAY-1997; 97US-0852824.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX L1 Y, Ruben SM;
XX
XX NPI; 1999-034722/03.
XX
XX P-PDB; AAW81577.
XX
XX New isolated human G-protein coupled receptors - used to develop
XX products for treating e.g. asthma; Parkinson's disease; heart
XX failure; osteoporosis; hypertension; psychoses; eating disorders or
XX cancers
XX
XX Claim 10; Fig 3A-B; 65pp; English.
XX
XX This cDNA encodes a EDG-1-like G-protein coupled receptor polypeptide.
XX The present sequence is deposited under the accession number ATCC No:
XX 209004. The invention provides two human G-protein coupled receptor
XX polypeptides. The polypeptides are human Epstein-Barr Virus (EBV)-induced
XX G-protein coupled receptor, designated EBV-2 polypeptide and a human
XX endohepeliun-differentiation gene (EDG) like G-protein coupled receptor,
XX designated EDG-1-like G-protein coupled receptor. Vectors comprising the
XX EBV-2 and EDG-1-like polypeptides encoding DNA can be used to transform
XX host cells for the recombinant production of the proteins. Agonists for

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CC G-protein coupled receptors can be used for the treatment of asthma,
CC Parkinson's disease, acute heart failure, hypotension, urinary retention
CC and osteoporosis. Antagonists can be used for the treatment of
CC hypertension, angina pectoris, myocardial infarction, ulcers, asthma,
CC allergies, psychoses, depression, migraine, vomiting, stroke, eating
CC disorders, migraine headaches, cancer and benign prostatic hypertrophy.
CC The products can also be used for detection, diagnosis and drug
CC screening.
XX
XX Sequence 1637 BP; 254 A; 551 C; 529 G; 303 T; 0 other;
SQ
Query Match 98.6%; Score 1139; DB 20; Length 1637;
Best Local Similarity 99.1%; Pred. No. 3,2e-182;
Matches 1145; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY 1 ATGAGCCGACAGGGGACCCCGTGGCCCGGAGTCCGCAACAGCTGCGCGCGCGG 60
DB 50 ATGAGCCGACAGGGGACCCCGTGGCCCGGAGTCCGCAACAGCTGCGCGCGCGG 109
QY 61 CACAGCCGCTCATTTGCTTGCACCTACACACTGAGCGCGCGCGCGCGCGG 120
DB 110 CACAGCCGCTCATTTGCTTGCACCTACACACTGAGCGCGCGCGCGCGG 169
QY 121 CCGAGGATGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGG 180
DB 170 CCGAGGATGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGG 229
QY 181 GTGCTGAGAACTGCTGCTGCTGCGCGCGCGCGCGCGCGCGCGCGG 240
DB 230 GTGCTGAGAACTGCTGCTGCTGCGCGCGCGCGCGCGCGCGCGCGG 289
QY 241 GTCTACTATGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
DB 290 GTCTACTATGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 349
QY 301 GCCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
DB 350 GCCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 409
QY 361 CGGAGGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
DB 410 CGGAGGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 469
QY 421 GGGAGCGCTTGTGCGCACATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
DB 470 GGGAGCGCTTGTGCGCACATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 529
QY 481 CGCGTCTACGCGCTTGTGCGCACATGCTGCTGCTGCTGCTGCTGCTGCTG 540
DB 530 CGCGTCTACGCGCTTGTGCGCACATGCTGCTGCTGCTGCTGCTGCTGCTG 589
QY 541 TTGCTGAGCTGAGAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
DB 590 TTGCTGAGCTGAGAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 649
QY 601 TCCAGGCGTACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
DB 650 TCCAGGCGTACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 709
QY 661 GCGCTCTATGAGGCGCATCTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
DB 710 GCGCTCTATGAGGCGCATCTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 769
QY 721 GCGGCGCGCGCGCAAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGG 780
DB 770 GCGGCGCGCGCGCAAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGG 829
QY 781 CTGCTGCTGCTGAGGCGCGCATCTTCCGCTGCTGCTGCTGCTGCTGCTGCTG 840
DB 830 TAGTGTGCTGAGGCGCGCATCTTCCGCTGCTGCTGCTGCTGCTGCTGCTG 889
QY 841 TTGGCGCCGAGATACCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGG 900
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Db 890 TGGGCCAGGATGCTGCGGGGATGAGCTGATCTTGCCCTGGCCCTCTCAACTGG 949
 QY 901 GCGGTCAACCCCATCATCTACTCTTCCGACAGGAGGTGTGACAGCCGTCTCAGC 960
 Db 950 GCGGTCAACCCCATCATCTACTCTTCCGACAGGAGGTGTGACAGCCGTCTCAGC 1009
 QY 961 TTCTCTGCTGCGGGGTCTCCGCGGAGATGCGAGGGCCCGGAGACTGCGGCCGG 1020
 Db 1010 TTCTCTGCTGCGGGGTCTCCGCGGAGATGCGAGGGCCCGGAGACTGCGGCCGG 1069
 QY 1021 GCGGTCAAGCTACTCTGAGGCTTCCACCCAGCAGCTCTCTGAGGCCAAGGACAGC 1080
 Db 1070 GCGGTCAAGCTACTCTGAGGCTTCCACCCAGCAGCTCTCTGAGGCCAAGGACAGC 1129
 QY 1081 TTTCGCGGCTCCGCTGCTGACCTTTGCGATGCGGAGCCCTGTCTCAGCATCTCAGC 1140
 Db 1130 TTTCGCGGCTCCGCTGCTGACCTTTGCGATGCGGAGCCCTGTCTCAGCATCTCAGC 1189
 QY 1141 GTGGGAGCATCTGA 1155
 Db 1190 GTGGGAGCATCTGA 1204

RESULT 10
 AAV68602
 ID AAV68602 standard; DNA; 1649 BP.

AAV68602;
 16-FEB-1999 (first entry)

Nucleotide sequence of an edg-1 receptor.

XX NEDG; edg-1-like receptor; stimulation; cell proliferation; cancer;
 KW genetic defect; sickle cell anaemia; agonist; antagonist; antibody;
 KW probe; ss.

OS Homo sapiens.

XX Key Location/Qualifiers
 FH 10..1539
 FT CDS
 FT /*tag= a
 FT /product= "edg-1-like receptor"
 FT /transl_except= (pos: 67..69, aa: Xaa)
 FT /transl_except= (pos: 85..87, aa: Xaa)
 FT /note= "Xaa= unknown"

XX MO9848016-A1.

XX 29-OCT-1998.

XX 17-APR-1998; 98WO-US07830.

XX 24-APR-1997; 97US-0845566.

XX (INCY-) INCYTE PHARM INC.

XX Au-Young J, Guegler KJ.

XX WPI; 1998-609989/51.

XX P-PSDB; AAM80955.

XX New Edg-1 like receptor. NEDG - useful, e.g. to stimulate cell
 PT proliferation and screen for antagonists to treat disorders of
 PT excessive cell proliferation such as cancers

XX Claim 4; Fig 1A-1E; 63pp; English.

XX This is the nucleotide sequence of an edg-1-like receptor (NEDG), used
 CC in the method of the invention. NEDG can be used to stimulate cell
 CC proliferation, especially by expressing encoding polynucleotides,
 CC either in vivo (e.g. to promote cell regeneration/differentiation) or
 CC in vitro (e.g. to stimulate cell proliferation for transplantation).

CC Such administration may be useful therapeutically, e.g. to stimulate
 CC proliferation of cells selected for their ability to fight an
 CC infection or a cancer, or correct a genetic defect, e.g. sickle cell
 CC anaemia. It can be used to screen for agonists (useful to
 CC treat/prevent disorders of abnormal cell growth and differentiation
 CC as above) and antagonists, and to generate antibodies. The antagonists
 CC can be combined with a suitable carrier in pharmaceutical compositions,
 CC useful to treat/prevent disorders of excessive cell proliferation,
 CC especially cancers. The NEDG-specific antibodies may be used directly
 CC as antagonists, or indirectly as a targeting or delivery mechanism
 CC to bring pharmaceutical agents to NEDG-expressing cells. They are
 CC also useful to diagnose conditions or diseases characterised by NEDG
 CC expression, and to monitor for therapeutic interventions. They are useful
 CC to produce antisense sequences for therapeutic administration to
 CC modulate/prevent NEDG expression. They may also be used to produce
 CC probes useful to detect related sequences, or for gene mapping.

SQ Sequence 1649 BP; 226 A; 539 C; 543 G; 318 T; 23 other;

Query Match 95.7%; Score 1104.8; DB 19; Length 1649;
 Best Local Similarity 99.2%; Pred. No. 1.7e-176;
 Matches 1150; Conservative 0; Mismatches 5; Indels 4; Gaps 4;

QY 1 ATGAACGCCACGCGGACCCCGGTGGCCCGAGTCTGCAACAGCTGGCGCGCGG 60
 Db 10 ATGAACGCCACGCGGACCCCGGTGGCCCGAGTCTGCAACAGCTGGCGCGCGG 69
 QY 61 CACAGCGCGCTCATTTTCTTGCACTACACCACTGCGCGCGCTGGCGCGCGG 120
 Db 70 CACAGCGCGCTCATTTTCTTGCACTACACCACTGCGCGCGCTGGCGCGCGG 129
 QY 121 CCGGAGATGCGCGCGCTGGCGCGCGCTGGCGCGCGCTGGCGCGCGG 180
 Db 130 CCGGAGATGCGCGCGCTGGCGCGCGCTGGCGCGCGCTGGCGCGCGG 189
 QY 181 GTGCTGAGAACTTGTGCTGTGCTGGCGCGCATCACCAGCCATGCGGTGCGAGCTGTG 240
 Db 190 GTGCTGAGAACTTGTGCTGTGCTGGCGCGCATCACCAGCCATGCGGTGCGAGCTGTG 249
 QY 241 GTCTACTATTGCTGCTGAGAACTACAGCAGTACGCTGCTCAACGCGCGCTTACTGT 300
 Db 250 GTCTACTATTGCTGCTGAGAACTACAGCAGTACGCTGCTCAACGCGCGCTTACTGT 309
 QY 301 GCCAAGCTGCTGCTGTCGCGGGGCGCCACACTTCCGTGTGGCGCGCGCCAGTGTCTTA 360
 Db 310 GCCAAGCTGCTGCTGTCGCGGGGCGCCACACTTCCGTGTGGCGCGCGCCAGTGTCTTA 369
 QY 361 CCGGAGGCGCTGCTTTCACCGCGCTGGCGCGCTTCCACCTGACCTGACCTGACCTGA 420
 Db 370 CCGGAGGCGCTGCTTTCACCGCGCTGGCGCGCTTCCACCTGACCTGACCTGACCTGA 429
 QY 421 GGGGAGCGCTTTGGACACCATGATGGCGCGGTGGCGGAGAGCGGGGCCAACAGACACAG 480
 Db 430 GGGGAGCGCTTTGGACACCATGATGGCGCGGTGGCGGAGAGCGGGGCCAACAGACACAG 489
 QY 481 CCGCTCTACGCGTTTCACTGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
 Db 490 CCGCTCTACGCGTTTCACTGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 549
 QY 541 TTGCTGGGCTGGAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
 Db 550 TTGCTGGGCTGGAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 609
 QY 601 TCCAAGGCGTCACTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
 Db 610 TCCAAGGCGTCACTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 669
 QY 661 GCGCTCTATGCGGCACTCTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
 Db 670 GCGCTCTATGCGGCACTCTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 729
 QY 721 GCGGCGCGCGCAAGGCGCGCGCTGCTGTAAGCGGTGCTGATGATCTGCTGCTGCTGCT 780

Db 730 GCGGCCCGCGAAGGCCCGCGCTGCTGAAGAGGCTGTGATGATCCTGCTGGCCTTC 789
 QY 781 CTGATGTGCTGGGGCCCACTCTTC-GGGCTGCTGCTGGCCGACGCTTTGGCTCCAACTT 839
 Db 790 CTGATGTGCTGGGGCCCACTCTTCGGGGCTGCTGCTGGCCGACGCTTTGGCTCCAACTT 849
 QY 840 CTGGGCCCCAGAGTACCTCGGGGGCATGAGTACCTCGGGCCCTGGCCGCTCCAACTC 899
 Db 850 CTGGGCCCCAGAGTACCTCGGGGGCATGAGTACCTCGGGCCCTGGCCGCTCCAACTC 909
 QY 900 GCGGCTCAACCCCATCATCTATCTCTCCGACGACAGGAGGTGTCAAGAGCCGTGCTCAG 959
 Db 910 GCGGCTCAACCCCATCATCTATCTCTCCGACGACGAGGAGGTGTCAAGAGCCGTGCTCAG 969
 QY 960 -CTTCCTCTGCTGGGGTGTCTCCGCTGAGGATGAGAGGCC-CGGGAGCTGCTGGCC 1017
 Db 970 CTTCTCTGCTGGGGTGTCTCCGCTGAGGATGAGAGGCCCGGGGAGCTGCTGGCC 1029
 QY 1018 CCGGCGCTGAGAGCTACTCCGAGACTTCC-ACACCGACAGCTCTCTGAGGCCAAGGGA 1076
 Db 1030 CCGGCGCTGAGAGCTACTCCGAGACTTCCAAACACGACAGCTCTCTGAGGCCAAGGGA 1089
 QY 1077 CAGCTTTGCGGGCTCCCGCTGCTCAGCTTCGAGTTCGAGTGGGAGACCCCTGTCCAGATCTC 1136
 Db 1090 CAGCTTTGCGGGCTCCCGCTGCTCAGCTTCGAGTTCGAGTGGGAGACCCCTGTCCAGATCTC 1149
 QY 1137 CAGCGTGCAGACATCTGA 1155
 Db 1150 CAGCGTGCAGACATCTGA 1168

RESULT 11

ID ABA05827 standard; cDNA: 4621 BP.
 AC ABA05827;

DT 15-MAR-2002 (first entry)
 DE Human Lyso-1 receptor coding sequence.

XX Human Lyso-1 receptor; G-protein coupled receptor; chromosome 11p;
 KW ED66 receptor; Gessler-Wilm's tumour; ss.

OS Homo sapiens.

FH Key Location/Qualifiers
 FT 1196..2222
 FT CDS /*tag- a
 product= "Lyso-1 receptor"

PN DE10007629-A1.

PD 23-AUG-2001.

PF 21-FEB-2000; 2000DE-1007629.

PR 21-FEB-2000; 2000DE-1007629.

PA (BRUE/) BRUESS M.
 PA (BOEN/) BOENISCH H.

PI Brues M, Boenisch H;

DR WPI; 2001-607848/70.

DR P-PSDB; ABB04481.

PT New gene encodes a polypeptide useful for diagnosing Gessler-Wilm's
 PT tumor, comprising the Lyso-1 receptor which is homologous to the ED66
 PT receptor -

PS Disclosure; Column 4; 4pp; German.

CC The present invention provides a human gene encoding a polypeptide
 CC comprising the Lyso-1 receptor, which is homologous to the ED66 receptor.
 CC The protein is a G-protein coupled receptor, and the gene is found on
 CC chromosome 11p. The sequences can be used to diagnose Gessler-Wilm's
 CC tumour. The present sequence is the coding sequence of the invention.

SO Sequence 4621 BP; 842 A; 1386 C; 1381 G; 1009 T; 3 other;

Query Match 77.4%; Score 894.2; DB 23; Length 4621;

Best Local Similarity 93.9%; Pred. No. 3,1e-141;

Matches 1085; Conservative 0; Mismatches 48; Indels 22; Gaps 14;

QY 1 ATGAAACCCACAGGGGACCCCGGGTGGCCCGAGTCTGCTCCAAAGCTGGCGCGGG 60
 Db 1196 ATGAAACCCACAGTGGACCCCGGGTGGCCCGAGTCTGCTCCAAAGCTGGCGCGGG 1255
 QY 61 CACAGCCGGCTCATTTGCTGCACTACAAACACATCGGGCGCGGGTGGCGCGGGGG 120
 Db 1256 CACAGCCGGCTCATTTGCTGCACTACAAACACATCGGG-CGGCTGGCCGGGGGGGG 1314
 QY 121 CCGGAGATGGCGGCTGGGGGCTCGGGGGCTGTGGTGGCCGCAAGCTGCTGTG 180
 Db 1315 CCGGAGATGGAGCGCTGGGAGCTGGGGGTGTGGT-----GCCGCAAGTCTGTG 1369
 QY 181 GTGCTGAGAACTTGGTGGTGGTGGGGGCGCATCAGACGACATGGGTGGAGCGCTGG 240
 Db 1370 GTGCTGAGAACTTGGTGGTGGTGGGGGCGCATCAGACGACATGGGTGGAGCGCTGG 1429
 QY 241 GTCTACTATTGCTGTGTAACATACGCTGAGTGAATGACCTGCTCAAGGCGCGCTTAC 300
 Db 1430 GTCTACTATTGCTGTGTAACATACGCTGAGTGAATGACCTGCTCAAGGCGCGCTTAC 1487
 QY 301 GCCAAGCTGCTGTGTGGGGGGCGCCACCTTCCGCTGTGGCGCGCCGCAAGTGTCTTA 360
 Db 1488 GCCAAGCTGCTGTGTGGGGGG-CGCGACCTTCTGTTGGGGCGCG-CCAAGTGTCTTA 1545
 QY 361 CCGGAGGGCTGCTGTTCACCGCCCTGGCGGCTCCACCTTCAAGCTGTCTTCACTGA 420
 Db 1546 CCGGAGGGCTGCTGTTCACCGCCCTGGCGGCTCCACCTTCAAGCTGTCTTCACTGA 1605
 QY 421 GGGGAGCGCTTTCACACATGTGTGGGGCGGTGGCCGAGAGCGGGGCCAAGACCAAG 480
 Db 1606 GGGGAGCGCTTTC-CACCAATGTGTGGGGCGGTGGAC---ACGTGGGGGCCAAGACCAAG 1661
 QY 481 CCGCTTACGGCTTTCATCGGCGCTGCTGCTGGCGGCGGCTGCTGGGATGTGGCT 540
 Db 1662 CCGCTTAC-GCTTTCATCGGCGCTGCTGCTGGCGGCGGCTGCTGGGATGTGGCT 1720
 QY 541 TTGCTGGGCTGGAATGCTGTGGCGCTTTCACCGCTGCTGCAAGCTTCTGCCCCCTTAC 600
 Db 1721 TTGCTGGGCTGGAATGCTGTGGCGCTTTCACCGCTGCTGCAAGCTTCTGCCCCCTTAC 1780
 QY 601 TCCAAAGCTTACATCTCTTTCGCTGTGATCTTCGCGGGCTGCTGGCCACATCATG 660
 Db 1781 TCCAAAGCTTACATCTCTTTCGCTGTGATCTTCGCGGGCTGCTGGCCACATCATG 1840
 QY 661 GGCCTCTATGGGCCATCTTCGCGGTGTGCAAGGCGCAGAGCCAGAGCCCAAGCCCA 720
 Db 1841 GGCCTCTATGGGCCATCTTCGCGGTGTGCAAGGCGCAGAGCCCAAGCCCA 1899
 QY 721 GCGGCGCGCGCAAGGCCCGGCTGCTGTAAGACGCTGTGATGATCTCTGTGGCTTC 780
 Db 1900 GCGTCC--GCCGCAAGCCCGCGGCTGCTGTAAGACGCTGTGATGATCTCTGTGGCTTC 1957
 QY 781 CTGATGTGCTGGGGCCCACTCTTGGGGCTGCTGGCGCGGCGAGCGTGTGGCTCCAACTC 840
 Db 1958 CTGATGTGCTGGGGCCCACTCTTGGGGCTGCTGGCGCGGCGAGTGTGGCTCCAACTC 2017
 QY 841 TGGGCCCAAGAGTACCTCGGGGATGAGTGAATGACTGTGGGCTGGCGGCTCTCAACTCG 900
 Db 2018 TGGGCCCAAGAGTACCTCGGGGATGAGTGAATGACTGTGGGCTGGCGGCTCTCAACTCG 2077
 QY 901 GCGGTCAACCCCATCATCTACTCTTCCGACAGAGGAGGTGTGCAAGCCGCTGCTAGC 960

[illegible]

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RESULT 12
AAx82790
ID    AAX82790 standard; DNA; 1161 BP.

```

DT 29-JUN-2000 (first entry)

DE Murine edg6 DNA.

KW edg6; murine; G-coupled receptor; endothelial differentiation gene;
 KW antiinflammatory; immunomodulatory; antimicrobial; antiallergic;
 KW cytoskeletal; gene therapy; inflammation; autoimmune disease; allergy
 KW tumor; leukemia; lymphoma; ss.

Mus sp. OS

PN DE19846979-A1

PD 23-MAR-2000.

PF - 13-OCT-1998; 98DE-1046979.

PR 11-SEP-1998; 98DE-1043240.

PA (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.

PI Graeler M, Bernhardt G, Lipp M,

DR WPI; 2000-258069/23

PT New human and murine G-coupled receptor EDG (endothelial
 PR differentiation gene) 6, useful for modulating inflammatory and immune
 PR reactions and for treatment of allergy or tumors -
 XX
 PS Claim 6; Page 8; 12pp; German.

CC This invention describes novel human and murine G-coupled receptors ED6
CC (endothelial differentiation gene) 6 (I and II). The products of the
CC invention have antiinflammatory, immunomodulatory, antimicrobial,
CC antiallergic and cytostatic activity. (I) and (II) are involved in signal
CC transduction. (I) / (II) and their fragments, variants and mutants or
CC binding partners, are used therapeutically to modulate the function of
CC blood and body cells, particularly for inhibition of acute and chronic
CC inflammation and to raise specific antibodies against them. They are used
CC as a source of diagnostic oligonucleotides and for gene therapy.
CC Antibodies against (I) and (II) are useful for diagnosis and optionally
CC when coupled to therapeutic agents, toxins or other antibodies, to
CC modulate immune and inflammatory responses for example immunological
CC defects such as inflammation, infection, autoimmune diseases, allergy,
CC tumors, leukemia and lymphoma. This sequence encodes the murine ED66
CC protein described in the method of the invention.

XX	09-OCT-1998;	98WO-US21315.
PF		
XX		
PR	10-OCT-1997;	97US-0061572.
XX		
PA	(LXRb-) LXR BIOTECHNOLOGY INC.	
XX		
PI	Erikson J, Goddard JG, Kiefer M;	
DR	WPI: 1999-277658/23.	
DR	P-PSDB; AAY05490.	
XX		
PT	Identification of (ant)agonists of LPA receptor EDG-2 for, e.g.	
PT	treating LPA signalling mediated diseases such as cellular apoptosis	
XX		
PS	Claim 1; Page 53-54; 63pp; English.	
XX		
CC	This sequence encodes human EDG-3.	
CC	The invention relates to methods of detecting (ant)agonist, inverse	
CC	agonist or allosteric modulators of the lysophosphatidic acid receptors	
CC	EDG-1, EDG-2, EDG-3, EDG-4, EDG-5, and PSP-24. The methods are used to	
CC	identify (ant)agonists and allosteric modulator of the lysophosphatidic	
CC	acid (LPA) EDG3 receptor, e.g. to treat LPA signalling mediated disease	
CC	such cellular apoptosis.	
XX		
Q	Sequence 1137 BP; 226 A; 362 C; 298 G; 251 T; 0 other;	

Query Match	22.28;	Score 256;	DB 20;	Length 1137;
Best Local Similarity	56.78;	Pred. No. 2.2e-34;		
Matches 513; Conservative	0;	Mismatches 385;	Indels 6;	Gaps 2;

QY	81	GCATCACAAACACATCGGAGCCGGCTGCGCCGGGCGGGGGGGCCGAGAGATGGCGCCCTGGG	140
Db	60	GCATTACCAATGACTGCGGAGAAATTGGCGGAGGCTCAAGAAAGGCCCTCCAGAGGCACAC	119
QY	141	GGCCCTGCGGGGGCTGTGCGGTGGCGCGGACCTGCTGGTGGTGGAGAACTTGTCTGGT	200
Db	120	GCTCACACACCTGCTCTTCTTGATCATCTCAGCTTCATGCTCTTGGAGAACCTGATGGT	179
QY	201	GCTGGCGGCGCATACACAGCAATGGCGGTGGCAGCGCTGGGTCTACTATTGCTGGTGA	260
Db	180	TTTATTATGCCATCTGGAAAAACAATAATTTCACACACGATGACTTTTTCATTGGCAA	239
QY	261	CATCACGCTGAGTACCTGCTCAACGGGCGGGGCCCTACTCTGGCCACAGCTGCTGTGCGG	320
Db	240	CTGTGCTCTGCGACACCTGGCTGGCGGCGATGCGTTACAAAGTACAATTTGTATGTCTGG	299
QY	321	GGCCCCGACCTTCCGTGTGGCGGCCGCCCAATGGTTCTTACGGGAGGCGCTGCTTTAC	380
Db	300	CAGAAGACGTTCAAGCTCTGTCTCCACAGTGTGGTTCTCAGGAGAGGCGATGTGTTGCT	359
QY	381	CGCCCTGAGCCGCTCCACACTTCAACCTGCTCTTCACTGCAAGGGGAGGGCTTTAGCCACAT	440
Db	360	GGCCCTTGGGGCGTCCACCTGCACCTTACTTGGCCATGGCATGAGGGGACACTTGAACAT	419
QY	441	GGTGGGCGCGGTGGCCCAAGAGCGGGGGCCACCAAGACAGCCGCGTCTACGGCTTATCGG	500
Db	420	GATCAAAATGAGGCTCTTA--CGAGCGCAACAAGAGGACACCGGCTCTCTCTCTGATCGG	476
QY	501	CCCTGCTGCGTGTGCGCCGCGGCTGTGGGAGATGCTCACTTCTGCGGCTGGAAGATGCGT	560
Db	477	GATGTGCTGGGCTCAATTGCTCTTCAACGCTGGCGGCCCTGSCCATTTCTGGGCTGGAACTGCGT	536
QY	561	GTGGCGCTTTAGCGCTGCTGCACAGCTTCTGCCCCCTTACTCCAAAGCGCTACTACTCTCTT	620
Db	537	GCACAATCTCCCTGACGCTCTCTTACATCTCGCCCTCTTACTCCAAAGTAAATTTGCTT	596
QY	621	CTGCGCTGGTATCTTCCCGCGGCGTCTGCGCACACATGAGCGCTCATATGGGCGCATCTT	680
Db	597	CTGCATCAGCATCTTCAAGGGGCATCCCTGGTGAACATGTATCTCTACGCAAGCATCTTA	656
QY	681	CCGCTGTGTGAGGCGCAAGGGGCAAGAGGCCCCACAGCCCGACGGCGCCCGCAAGGCCCG	740

Db	657	CTTCCTGGTGAAGTCCAGACACCCCTTAAGGTGGCCACACACAACTCCGAGCGGTTCAT	716
QY	741	CÇGGCTGCTGAAGACGGTGGTCTGATGATCTGCTGGCCCTTCCTGGTGTGCTGGGGCCCACT	800
Db	717	GGCACTGTCTGGGACCGGTGGTGATTTGGTGAGGCGTTTCATGGCCCTGGCTGGTGCCCACT	776
QY	801	CTTGGGGCTGTGGTGGGGCCGACGCTTTGGGTCCAACTCTGGGGCCCAAGAGTAACCGGG	860
Db	777	CTTCATCCTCTTCTCATATATG--TGGCTGCAGGGTGCAGGCCGTGCCCACTCCTCTT	833
QY	861	GGGCATGCACTGATCCTGCGCCCTGGCCGCTTCCTAACCTGGCGGTCAACCCCATCATTA	920
Db	834	CAAGGCTCAGTGGTTCATCGGTGGGTGTGCCTCAATCCGCCATGAACCCGGTCATCTA	893
QY	921	CTCCCTCCGCGCAGGAGGAGGTGTGCACAGGCCGTGCTAGTCTTCCTCGCGCGCGGGTGTCT	980
Db	894	CACGCTGGCCAGCAAGAGATGCGCGCGGCCCTTCTTCGCTGTGTGTGCACACTGCTGGT	953
QY	981	CCGG 984	
Db	954	CAGG 957	

```

RESULT 15
AAS00258
ID      AAS00258 standard; DNA; 1137 BP.

```

AC	AAS00258;
XX	
DT	11-MAY-2001 (first entry)

DE LPA receptor-related DNA sequence #2.

KM LPA receptor: ENG-2: lysophosphatidic acid: phospholipid: tumour;
KM cell signalling: MAP kinase: LPA modulator; neurodegenerative disease;
KM Alzheimer's disease; Parkinson's disease; neuron damage; apoptosis;
KM ischaemic heart disease; vital; HIV; inflammatory bowel disease;
KM organ transplant; human; ds.

OS Homo sapiens.

key	Location/Qualifiers
FH	1.1137
FT	/*tag= a
FT	

PN W0200112838-A2.

PD 22-FEB-2001.

PF 11-AUG-2000; 2000WO-US22101.

PR 18-AUG-1999; 99US-0376399.

PA (ATAI-) ATAIRGIN TECHNOLOGIES INC.

PI Erickson J, Goddard JG, Kiefer M, Picker D;

DR WPI; 2001-226550/23.

PT Modulating activity of a lysophosphatidic acid or its receptor for
PT treating tumours, viral diseases, involves introducing to LPA or its
PT receptor a composition containing diol, epoxide or phosphate compound
PT -
XX
DS Disclosure; Page 78-79; 89pp; English.

CC The sequence represents the LPA receptor-related sequence #2 used during
CC analysis of lysophosphatidic acid receptor (LPA), Edg-2. The sequence is
CC given in the specification but no further information is given. LPA is a
CC phospholipid found in a variety of plant and animal products. Edg-2 is
CC involved in cell signaling through activation of a Map kinase cascade
CC dependent reporter. Modulating the activity of a lysophosphatidic acid
CC (LPA) or LPA receptor (Edg-2) involves introducing a composition

Qy	181	GTGCTGAGAACTTCTCTGTCTGTCTGGCGGCATATACCAGCCATATCGGTGCGCAGCTGG	240
Dp	202	GTCCTGGAAACATTCTCTGTGTCTGGCGGCATATACCAGCCATATCGGTGCGCAGCTGG	261
Qy	241	GTCCTATTGTGCTGGTGAACATACAGCTAGTAGACTCTCTACAGGGGCGGCTTACTAG	300
Dp	262	GTCCTATTGTGCTGGTGAACATACAGCTAGTAGACTCTCTACAGGGGCGGCTTACTAG	321
Qy	301	GCCAAAGTCTCTCTGCGGGGGCCCGACCTTCCGCTGTGGGCCCGCCCAATGGTTCTTA	360
Dp	322	GCCAAAGTCTCTCTGCGGGGGCCCGACCTTCCGCTGTGGGCCCGCCCAATGGTTCTTA	381
Qy	361	CGGAGAGGCGCTCTTTCACGCGCCCTGGCCGCGCTCCACCTTTCAGCTCTTCTACTGGA	420
Dp	382	CGGAGAGGCGCTCTTTCACGCGCCCTGGCCGCGCTCCACCTTTCAGCTCTTCTACTGGA	441
Qy	421	GGGAGAGCGCTTGGACACATAGTGGCGCGGTGGCGGAGAGCGGGGCGCCACAGACACAG	480
Dp	442	GGGAGAGCGCTTGGACACATAGTGGCGCGGTGGCGGAGAGCGGGGCGCCACAGACACAG	501
Qy	481	CGGCTTACGCGCTTATCGGCTCTGCTGTGGCTGTGGCCCGCGCGCTGTGGGATGTGCGCT	540
Dp	502	CGGCTTACGCGCTTATCGGCTCTGCTGTGGCTGTGGCCCGCGCGCTGTGGGATGTGCGCT	561
Qy	541	TTGCTGTGGCTGGAAATGTGCTGTGGCTTTTGAACGCTGTCTCAGAGCTTTCGCCCTTAC	600
Dp	562	TTGCTGTGGCTGGAAATGTGCTGTGGCTTTTGAACGCTGTCTCAGAGCTTTCGCCCTTAC	621
Qy	- 601	TTCAAAGCTTAATCTCTTCTGTGCTGTGTATTTTGGCGGCTCTGTGGCCACCATATAG	660
Dp	622	TTCAAAGCTTAATCTCTTCTGTGCTGTGTATTTTGGCGGCTCTGTGGCCACCATATAG	681
Qy	661	GGCCTTATGTGGGCGCATTTTCGCGCTGTGTGACAGCCAGCGGCGAGAAAGGCCACAGCCCA	720
Dp	682	GGCCTTATGTGGGCGCATTTTCGCGCTGTGTGACAGCCAGCGGCGAGAAAGGCCACAGCCCA	741
Qy	721	GCGGCGCGCGGAGAGCCCGCGCGCTGTGAAGAGCTGTATGATATGATCTGTGGCGCTTC	780
Dp	742	GCGGCGCGCGGAGAGCCCGCGCGCTGTGAAGAGCTGTATGATATGATCTGTGGCGCTTC	801
Qy	781	CTGCTGTGCTGGGGCCCACTTCTTGGGCTGTCTGTGTGGCGAGCTCTTTGGCTCCAACTTC	840
Dp	802	CTGCTGTGCTGGGGCCCACTTCTTGGGCTGTCTGTGTGGCGAGCTCTTTGGCTCCAACTTC	861
Qy	841	TGGGCGCCAGAGTATCTCCGCGGCGAGTGAATGATCTTGGCCCTGTGGCGTCTCAACTGS	900
Dp	862	TGGGCGCCAGAGTATCTCCGCGGCGAGTGAATGATCTTGGCCCTGTGGCGTCTCAACTGS	921
Qy	901	GCGGTAAACCCATATATCTCTTCCGAGAGAGGAGATGTGTGAAGCCGTGTCTACG	960
Dp	922	GCGGTAAACCCATATATCTCTTCCGAGAGAGGAGATGTGTGAAGCCGTGTCTACG	981
Qy	961	TTCTCTGTGCGGGGTGTCTCGGCTGGGATCGAGGGCCCGGGAGTGTGCTGGCCCG	1020
Dp	982	TTCTCTGTGCGGGGTGTCTCGGCTGGGATCGAGGGCCCGGGAGTGTGCTGGCCCG	1041
Qy	1021	GCGGTGAGAGCTCATCTCCGGAGCTTCCACACCGAAGTCTGTGAAGGCCAAAGGAGACG	1080
Dp	1042	GCGGTGAGAGCTCATCTCCGGAGCTTCCACACCGAAGTCTGTGTAGGCCAAAGGAGACG	1101
Qy	1081	TTTTGCGGCTCCCGCTGCGCTAGCTTTTGAGATGGGAGCCCTGTCTCCAGCATCTCCAG	1140
Dp	1102	TTTTGCGGCTCCCGCTGCGCTAGCTTTTGAGATGGGAGCCCTGTCTCCAGCATCTCCAG	1161
Qy	1141	GTCGAGAGCATCTGA 1155	
Dp	1162	GTCGAGAGCATCTGA 1176	

Query Match	Best Local Similarity	100.0%	Score 1155	DB 12	Length 1877
Matches 1155	Conservative	0	Mismatches	0	Gaps 0
1	ATGAACGCCACGGGGAGCCCGGGTGGCCCCCGAGTCTTCCCAACAGCTGGCGCGCGCGG	60			
284	ATGAACGCCACGGGGAGCCCGGGTGGCCCCCGAGTCTTCCCAACAGCTGGCGCGCGCGG	143			
61	CACAGCGGGCTCATTTCTGCACTACAAACACATCGGGCGGGCTGGCGCGCGCGCGCGG	120			
344	CACAGCGGGCTCATTTCTGCACTACAAACACATCGGGCGGGCTGGCGCGCGCGCGCGG	403			
121	CCGAGAGATGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGG	180			
404	CCGAGAGATGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGG	463			
181	GTGTGGAGAACTTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG	240			
464	GTGTGGAGAACTTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG	523			
241	GTCTACTATTGCTCGGTGTAACATCAAGCTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA	300			
524	GTCTACTATTGCTCGGTGTAACATCAAGCTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA	583			
301	GCCACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	360			
584	GCCACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	643			
361	CGGAGAGGCGCTGCTCTTTCACCGCGCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG	420			
644	CGGAGAGGCGCTGCTCTTTCACCGCGCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG	703			
421	GGGAGAGGCGCTTTCACCAATGCTGGCGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGG	480			
704	GGGAGAGGCGCTTTCACCAATGCTGGCGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGG	763			
481	CGGCTCTAGGGCTTTCACCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	540			
764	CGGCTCTAGGGCTTTCACCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	823			
541	TTGGTGGGCTGGAGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	600			
824	TTGGTGGGCTGGAGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	883			
601	TTCAAGGCGCTTTCACCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	660			
884	TTCAAGGCGCTTTCACCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	943			
661	GGGCTCTATGGGCGCTTTCACCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	720			
944	GGGCTCTATGGGCGCTTTCACCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1003			
721	GGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	780			
1004	GGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	1063			
781	CTGGTGGTGGTGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	840			

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Db 1064 CTGGTGTCTGGGGCCCACTCTTGGGCTGCTGTCGCGCCGACGTCCTTGGCTCCAACTTC 1123
Qy 841 TGGGGCCGAGAGTACCTTCGCGGGGATGAGATCTCTGGCCCTGGCCCTCTCAACACG 900
Db 1124 TGGGGCCGAGAGTACCTTCGCGGGGATGAGATCTCTGGCCCTGGCCCTCTCAACACG 1183
Qy 901 GGGGTCAACCCCATCATCTACTCTCTCCGAGCAGGAGAGTGTGACAGACCCGCTGCTCAGC 960
Db 1184 GGGGTCAACCCCATCATCTACTCTCTCCGAGCAGGAGAGTGTGACAGACCCGCTGCTCAGC 1243
Qy 961 TTCTCTGCTGCGGGTGTCTCTCCGCTGGCATGCGAGGGCCGCGGAGCTGCTGGCCCGG 1020
Db 1244 TTCTCTGCTGCGGGTGTCTCTCCGCTGGCATGCGAGGGCCGCGGAGCTGCTGGCCCGG 1303
Qy 1021 GCGGTGAGGGCTCACTCCGAGCTTCCACCCAGCAGAGCTCTCTAGAGCCAAAGGAGCAGC 1080
Db 1304 GCGGTGAGGGCTCACTCCGAGCTTCCACCCAGCAGAGCTCTCTAGAGCCAAAGGAGCAGC 1363
Qy 1081 TTTCCGCGGCTCCCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140
Db 1364 TTTCCGCGGCTCCCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1423
Qy 1141 GTGCGAGCATCTGA 1155
Db 1424 GTGCGAGCATCTGA 1438

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RESULT 3
US-09-731-030A-10
; Sequence 10, Application US/09731030A
; Patent No. US20020142375A1
; GENERAL INFORMATION:
; APPLICANT: MUNROE, Donald G.
; APPLICANT: GUPTA, Ashwani K.
; APPLICANT: ZASTAMNY, Roman L.
; TITLE OF INVENTION: MAMMALIAN EDG-7 RECEPTOR HOMOLOGS
; FILE REFERENCE: 8074-0015
; CURRENT APPLICATION NUMBER: US/09/731, 030A
; PRIOR FILING DATE: 1998-12-29
; PRIOR APPLICATION NUMBER: 60/070,184
; PRIOR FILING DATE: 1997-12-30
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 10
; LENGTH: 2270
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (16)..(1170)
US-09-731-030A-10

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Query Match 100.0%; Score 1155; DB 10; Length 2270;
Best Local Similarity 100.0%; Pred. No. 5, 2e-206; Indels 0; Gaps 0;
Matches 1155; Conservative 0; Mismatches 0;

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Qy 1 ATGAAGCCACGCGGAGCCCGGATGAGCCCGAGTCTGCCAACAGCTGAGCGGCGGCGG 60
Db 16 ATGAAGCCACGCGGAGCCCGGATGAGCCCGAGTCTGCCAACAGCTGAGCGGCGGCGG 75
Qy 61 CAGAGCGGCTCATTTGTTCTGCACTACAAACACTGCGGCGGCTGGCCGCGGCGGCGG 120
Db 76 CAGAGCGGCTCATTTGTTCTGCACTACAAACACTGCGGCGGCTGGCCGCGGCGGCGG 135
Qy 121 CCGAGAGATGCGGCTGAGGCGCCCTGCGGGGCTGTGAGTGGCCGACACTGCTGAGTG 180
Db 136 CCGAGAGATGCGGCTGAGGCGCCCTGCGGGGCTGTGAGTGGCCGACACTGCTGAGTG 195
Qy 181 GTGCTGGAAGACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
Db 196 GTGCTGGAAGACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 255

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Qy 241 GTCTACTATGCTGCTGTAACATACAGCTGAGTGAAGTCTGACAGGCGGCGCTACTG 300
Db 256 GTCTACTATGCTGCTGTAACATACAGCTGAGTGAAGTCTGACAGGCGGCGGCGCTACTG 315
Qy 301 GCCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
Db 316 GCCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 375
Qy 361 CCGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
Db 376 CCGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 435
Qy 421 GGGAGAGCTTTTGGCACCATGATGATGATGATGATGATGATGATGATGATGATGATG 480
Db 436 GGGAGAGCTTTTGGCACCATGATGATGATGATGATGATGATGATGATGATGATGATG 495
Qy 481 CCGCTCTACGCTTACATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
Db 496 CCGCTCTACGCTTACATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 555
Qy 541 TTCTGCGCTGGAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
Db 556 TTCTGCGCTGGAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 615
Qy 601 TCCAGAGCTTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
Db 616 TCCAGAGCTTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 675
Qy 661 GGCCTCTATGAGGCTATCTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
Db 676 GGCCTCTATGAGGCTATCTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 735
Qy 721 GCGGCGCCCGCAGAGGCGCGCGCTGCTGTAAGAGCTGCTGTAAGTCTGCTGCTGCTGCT 780
Db 736 GCGGCGCCCGCAGAGGCGCGCGCTGCTGTAAGAGCTGCTGTAAGTCTGCTGCTGCTGCT 795
Qy 781 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
Db 796 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 855
Qy 841 TGGGCGCCAGAGTACCTGCGGGGATGAGATCTGAGATCTGAGATCTGAGATCTGAGATCT 900
Db 856 TGGGCGCCAGAGTACCTGCGGGGATGAGATCTGAGATCTGAGATCTGAGATCTGAGATCT 915
Qy 901 GCGGTCAACCCCATCATCTACTCTTCCGAGCAGGAGAGTGTGAGAGCGTGTGCTGAGC 960
Db 916 GCGGTCAACCCCATCATCTACTCTTCCGAGCAGGAGAGTGTGAGAGCGTGTGCTGAGC 975
Qy 961 TTCTCTGCTGCGGCTGTCTCGGCTGGCATGCGAGGGCCGCGGAGCTGCTGAGCCCGG 1020
Db 976 TTCTCTGCTGCGGCTGTCTCGGCTGGCATGCGAGGGCCGCGGAGCTGCTGAGCCCGG 1035
Qy 1021 GCGGTGAGGGCTCATCTGCGGAGCTTCCACCCAGCAGAGCTCTGAGGCGCAAGGAGCAG 1080
Db 1036 GCGGTGAGGGCTCATCTGCGGAGCTTCCACCCAGCAGAGCTCTGAGGCGCAAGGAGCAG 1095
Qy 1081 TTTGCGGCTCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140
Db 1096 TTTGCGGCTCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1155
Qy 1141 GTGCGAGCATCTGA 1155
Db 1156 GTGCGAGCATCTGA 1170

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RESULT 4
US-09-731-030A-12
; Sequence 12, Application US/09731030A
; Patent No. US20020142375A1
; GENERAL INFORMATION:
; APPLICANT: MUNROE, Donald G.
; APPLICANT: GUPTA, Ashwani K.
; APPLICANT: ZASTAMNY, Roman L.

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: TITLE OF INVENTION: MAMMALIAN EDG-7 RECEPTOR HOMOLOGS
: FILE REFERENCE: 8074-0015
: CURRENT APPLICATION NUMBER: US/09/731,030A
: CURRENT FILING DATE: 1998-12-29
: PRIOR APPLICATION NUMBER: 60/070,184
: PRIOR FILING DATE: 1997-12-30
: NUMBER OF SEQ ID NOS: 21
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 12
: LENGTH: 1176
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (13)..(1167)
: US-09-731-030A-12

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Query Match          99.7%; Score 1151.8; DB 10; Length 1176;
Best Local Similarity 99.8%; Pred. No. 2e-205;
Matches 1153; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 1 ATGAAGCCAGCGGGACCCCGTGGCCCGAGTCCCTGCCACAGCTGGGGCGGGGG 60
DB 13 ATGAAGCCAGCGGGACCCCGTGGCCCGAGTCCCTGCCACAGCTGGGGCGGGGG 72
QY 61 CACAGCCGCTCATTTGTTCTGACTACACACTGGCGGCTGGCGGCGGGGG 120
DB 73 CACAGCCGCTCATTTGTTCTGACTACACACTGGCGGCTGGCGGCGGGGG 132
QY - 121 CCGAGAGATGGGGGCTGGGGGCTGGGGGCTGCTGGTGGCGGCGGCTGGT 180
DB 133 CCGAGAGATGGGGGCTGGGGGCTGGGGGCTGCTGGTGGCGGCGGCTGGT 192
QY 181 GTGCTGAGAAATTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 240
DB 193 GTGCTGAGAAATTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 252
QY 241 GTCTACTATTTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 300
DB 253 GTCTACTATTTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 312
QY 301 GCCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 360
DB 313 GCCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 372
QY 361 CCGGAGGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 420
DB 373 CCGGAGGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 432
QY 421 GGGGAGCGCTTTGCCACCATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 480
DB 433 GGGGAGCGCTTTGCCACCATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 492
QY 481 CCGGCTACTAGGCTTCATGGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 540
DB 493 CCGGCTACTAGGCTTCATGGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 552
QY 541 TTGCTGAGCTGAGACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 600
DB 553 TTGCTGAGCTGAGACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 612
QY 601 TCCAGAGCGCTACTATTTGTTCTGCTGTGTGTGTGTGTGTGTGTGTGTGT 660
DB 613 TCCAGAGCGCTACTATTTGTTCTGCTGTGTGTGTGTGTGTGTGTGTGTGT 672
QY 661 GGGCTCTAGGAGGCGCTTCCTGGGCTGTGTGTGTGTGTGTGTGTGTGTGT 720
DB 673 GGGCTCTAGGAGGCGCTTCCTGGGCTGTGTGTGTGTGTGTGTGTGTGTGT 732
QY 721 GCGGCGCGCGCGAGGCGCGCGCGCTGTGTGTGTGTGTGTGTGTGTGTGT 780
DB 733 GCGGCGCGCGCGAGGCGCGCGCGCTGTGTGTGTGTGTGTGTGTGTGTGT 792

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QY 781 CTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 840
DB 793 CTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 852
QY 841 TGGGCCCCAGAGTACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900
DB 853 TGGGCCCCAGAGTACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 912
QY 901 GCGGTCACCCCATCATCTACTTCTTCCGAGCAGGAGGTGTGTGTGTGTGT 960
DB 913 GCGGTCACCCCATCATCTACTTCTTCCGAGCAGGAGGTGTGTGTGTGTGT 972
QY 961 TTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1020
DB 973 TTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1032
QY 1021 GCGGTCAGAGCTCACTCCGAGCTTCCACCCAGCAGCAGCTCTGTAGGCCAAGGAGCAGC 1080
DB 1033 GCGGTCAGAGCTCACTCCGAGCTTCCACCCAGCAGCAGCTCTGTAGGCCAAGGAGCAGC 1092
QY 1081 TTTCGGGCGCTCCCGCTGCTGAGCTTTCGATGTGTGTGTGTGTGTGTGTGT 1140
DB 1093 TTTCGGGCGCTCCCGCTGCTGAGCTTTCGATGTGTGTGTGTGTGTGTGTGT 1152
QY 1141 GTGCGGAGCATCTGA 1155
DB 1153 GTGCGGAGCATCTGA 1167

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RESULT 5
US-09-731-030A-14
: Sequence 14, Application US/09731030A
: Patent No. US20020142375A1
: GENERAL INFORMATION:
: APPLICANT: MUNROE, Donald G.
: APPLICANT: GUPTA, Ashwani K.
: APPLICANT: ZASTAWNY, Roman L.
: TITLE OF INVENTION: MAMMALIAN EDG-7 RECEPTOR HOMOLOGS
: FILE REFERENCE: 8074-0015
: CURRENT APPLICATION NUMBER: US/09/731,030A
: PRIOR FILING DATE: 1998-12-29
: PRIOR APPLICATION NUMBER: 60/070,184
: PRIOR FILING DATE: 1997-12-30
: NUMBER OF SEQ ID NOS: 21
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 14
: LENGTH: 1152
: TYPE: DNA
: ORGANISM: Homo sapiens
: US-09-731-030A-14

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Query Match          99.5%; Score 1148.8; DB 10; Length 1152;
Best Local Similarity 99.8%; Pred. No. 7.1e-205;
Matches 1150; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 1 ATGAAGCCAGCGGGACCCCGTGGCCCGAGTCCCTGCCACAGCTGGGGCGGG 60
DB 1 ATGAAGCCAGCGGGACCCCGTGGCCCGAGTCCCTGCCACAGCTGGGGCGGG 60
QY 61 CACAGCGGCTCATTTGTTCTGCTACTACACACTGTGGGCGGCTGGCGGCGGG 120
DB 61 CACAGCGGCTCATTTGTTCTGCTACTACACACTGTGGGCGGCTGGCGGCGGG 120
QY 121 CCGGAGAGTGGGGGCTGGGGGCTGGGGGCTGTGTGTGTGTGTGTGTGTGTGT 180
DB 121 CCGGAGAGTGGGGGCTGGGGGCTGGGGGCTGTGTGTGTGTGTGTGTGTGTGT 180
QY 181 GTGCTGAGAACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 240
DB 181 GTGCTGAGAACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 240
QY 241 GTCTACTATTTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 300

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Db 241 GTCTACTATTGCTGTGTGAACATACGCTGAGTGAACCTGCTCACGGGCGGCGCTTACTG 300
QY 301 GCGAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 360
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 301 GCGAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 360
QY 361 GCGGAGGGGCTGCTCTTTCACCGGCGCTGCGGCGCTGCGGCGCTGCGGCGCTGCGGCGCT 420
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 361 GCGGAGGGGCTGCTCTTTCACCGGCGCTGCGGCGCTGCGGCGCTGCGGCGCTGCGGCGCT 420
QY 421 GGGGAGGCTTTTGGACCAATGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 480
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 421 GGGGAGGCTTTTGGACCAATGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 480
QY 481 GCGCTCTACAGGCTTACATCGGCGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 540
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 481 GCGCTCTACAGGCTTACATCGGCGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 540
QY 541 TTGCTGGGCTGTGAACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 600
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 541 TTGCTGGGCTGTGAACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 600
QY 601 TTCAAAGGCTACATCTTCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 660
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 601 TTCAAAGGCTACATCTTCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 660
QY 661 GGCCTCTATGGGCGCATCTTCCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 720
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 661 GGCCTCTATGGGCGCATCTTCCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 720
QY 721 GCGGCGCGCGCGCAAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 780
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 721 GCGGCGCGCGCGCAAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 780
QY 781 CTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 840
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 781 CTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 840
QY 841 TGGGCGCGAGGATCTGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 900
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 841 TGGGCGCGAGGATCTGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 900
QY 901 GCGGCTCAACCCCATCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 960
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 901 GCGGCTCAACCCCATCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 960
QY 961 TTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1020
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 961 TTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1020
QY 1021 GCGGCTCAACCCCATCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1080
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1021 GCGGCTCAACCCCATCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1080
QY 1081 TTTGCGGCGCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
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Db 1081 TTTGCGGCGCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
QY 1141 GTGGGAGGAGCATC 1152
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Db 1141 GTGGGAGGAGCATC 1152

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; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 08/852,824
; PRIOR FILING DATE: 1997-05-07
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1637
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (50)..(1201)
US-09-827-937A-3

Query Match      98.9%; Score 1142.2; DB 10; Length 1637;
Best Local Similarity 99.3%; Pred. No. 1,2e-203;
Matches 1147; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 ATGAACGCCACAGGGGACCCCGGTGGCCCGCGAGTCTGTGCCAACAGCTGGCGGGCGGG 60
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 50 ATGAACGCCACAGGGGACCCCGGTGGCCCGCGAGTCTGTGCCAACAGCTGGCGGGCGGG 109
QY 61 CACAGCGCGCTATGTTTGTGCACTACACACTGCGGCGCGGCTGGCGGGCGGGGGGG 120
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 110 CACAGCGCGCTATGTTTGTGCACTACACACTGCGGCGCGGCTGGCGGGCGGGGGGG 169
QY 121 CCGGAGATGGCGGCTGTGGGGGCGCTGCGGGGGCTGTGGTGGCCGCAAGCTGCTGCTG 180
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 170 CCGGAGATGGCGGCTGTGGGGGCGCTGCGGGGGCTGTGGTGGCCGCAAGCTGCTGCTG 229
QY 181 GTGCTGAGAACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 240
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 230 GTGCTGAGAACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 289
QY 241 GTCTACTATTGCTGTGTGAACATACGCTGAGTGAACCTGCTACGCGGCGGCGCTTACTG 300
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 290 GTCTACTATTGCTGTGTGAACATACGCTGAGTGAACCTGCTACGCGGCGGCGCTTACTG 349
QY 301 GCGAAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 360
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 350 GCGAAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 409
QY 361 GCGGAGGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 420
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 410 GCGGAGGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 469
QY 421 GGGGAGGCTTTTGGACCAATGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 480
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 470 GGGTGTGCGCTTTGCGACCATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 529
QY 481 GCGGCTCAACCCCATCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 540
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 530 GCGGCTCAACCCCATCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 589
QY 541 TTTGCGGCGCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 590 TTTGCGGCGCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 649
QY 601 TTTGCGGCGCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 650 TTTGCGGCGCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 709
QY 661 GGCCTCTATGGGCGCATCTTCCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 720
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 710 GGCCTCTATGGGCGCATCTTCCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 769
QY 721 GCGGCGCGCGCGCAAGGCGCGCGCGCTGCTGAAGAGGCTGATGATCTGCTGCTGCTGCTGCT 780
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 770 GCGGCGCGCGCGCAAGGCGCGCGCGCTGCTGAAGAGGCTGATGATCTGCTGCTGCTGCTGCT 829
QY 781 CTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 840
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 830 TTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 889

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RESULT 6
US-09-827-937A-3
; Sequence 3, Application US/09827937A
; Patent No.: US20020052043A1
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Human G-Protein Coupled Receptors
; FILE REFERENCE: 1488.122003
; CURRENT APPLICATION NUMBER: US/09/827,937A

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OY 841 TGGGCCAGGAGTACCTGCGGGGCGATGAGACTGAGTCTGGCCCTGGCCGTCCTCACTCG 900
Db 890 TGGGCCAGGAGTACCTGCGGGGCGATGAGACTGAGTCTGGCCCTGGCCGTCCTCACTCG 949
OY 901 GCGGTCAACCCCATCATCTACTCTCTCCGACAGAGAGTGTGTGACAGCCGTCGTAGC 960
Db 950 GCGGTCAACCCCATCATCTACTCTCTCCGACAGAGAGTGTGTGACAGCCGTCGTAGC 1009
OY 961 TTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1020
Db 1010 TTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1069
OY 1021 GCCGTGAGGCTCAGTCCGAGGCTTCCAGCAGCAGAGTCTGTAGAGGCAAGGAGACAGC 1080
Db 1070 GCCGTGAGGCTCAGTCCGAGGCTTCCAGCAGCAGAGTCTGTAGAGGCAAGGAGACAGC 1129
OY 1081 TTTTGGGGGCTCCGCTCCGCTCAGCTTTGGGATGCGGGAGCCCTGTCCAGATCTCCAGC 1140
Db 1130 TTTTGGGGGCTCCGCTCCGCTCAGCTTTGGGATGCGGGAGCCCTGTCCAGATCTCCAGC 1189
OY 1141 GTCCGAGACATCTGA 1155
Db 1190 GTCCGAGACATCTGA 1204

RESULT 7
US-09-917-508-1
; Sequence 1, Application US/09917508
; Patent No. US20020137136A1
; GENERAL INFORMATION:
; APPLICANT: TSUI, Ping
; TITLE OF INVENTION: Rat G Protein Coupled Receptor, EDG6
; FILE REFERENCE: GP-70715
; CURRENT APPLICATION NUMBER: US/09/917, 508
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/222, 259
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1161
; TYPE: DNA
; ORGANISM: RAT
US-09-917-508-1

Query Match 65.28; Score 752.8; DB 10; Length 1161;
Best Local Similarity 79.48; Pred. No. 1,6e-131;
Matches 918; Conservative 0; Mismatches 232; Indels 6; Gaps 2;
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OY 358 CTACGAGAGGCGCTGCTCTTCAACCGCCCTGCGCGCTTCACCTTCAAGCTGCTTCACT 417
Db 367 CTGCGGAGAGGCGCTGCTCTTCAACCGCCCTGCGCGCTTCACCTTCAAGCTGCTTCACT 426
OY 418 GCAGGGAGGCGCTTTCACCATAGTGTGCGGCGGTGCGGAGAGGCGGCGGCGGCGGAGAGC 477
Db 427 GCGGCGAGGCGCTTTCACCATAGTGTGCGGCGGTGCGGAGAGGCGGCGGCGGCGGAGAGC 483
OY 478 AGCGGCTCTACGCTTCACTGCGCTCTCTGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTG 537
Db 484 AGCGGCTCTACGCTTCACTGCGCTCTCTGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTG 543
OY 538 CCTTGTGCTGAGGAGTGAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 597
Db 544 CCTTGTGCTGAGGAGTGAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 603
OY 598 TACTTCAAGGCGCTACATCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 657
Db 604 TACTTCAAGGCGCTACATCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 663
OY 658 ATGGGCTCTATGAGGCGCATCTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 717
Db 664 CTGAGCTCTACGAGGCGCATCTTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 723
OY 718 CCAGGCGCGCGCGCGCAAGGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 777
Db 724 CCTCTGCGCGCGCGCGCAAGGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 783
OY 778 TTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 837
Db 784 TTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 843
OY 838 CTGTGCGCGCGCGCGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 897
Db 844 GTCTGCGCGCGCGCGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 903
OY 898 TCGCGGCTCAACCCCATCATCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 957
Db 904 TCAGCAGTCAATCCTCTCAATCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 963
OY 958 AGCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1017
Db 964 AGCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1023
OY 1018 CGGCGCGTCAAGGCTCAGTCCGAGGCTTCCAGCAGCAGAGTCTGTGAGGCGCAAGGAGC 1077
Db 1024 CGGATCACCGAGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1083
OY 1078 AGCTTGTGCGGCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1137
Db 1084 AGCTTGTGCGGCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1143
OY 1138 AGCGTGGGAGGACATCT 1153
Db 1144 AGCATCCGCAAGCGCT 1159

RESULT 8
US-09-731-030A-20
; Sequence 20, Application US/09731030A
; Patent No. US20020142375A1
; GENERAL INFORMATION:
; APPLICANT: MURROE, Donald G
; APPLICANT: GUPFA, Ashwani K.
; APPLICANT: ZASTAWNY, Roman L.
; TITLE OF INVENTION: MAMMALIAN EDG-7 RECEPTOR HOMOLOGS
; FILE REFERENCE: 8074-0015
; CURRENT APPLICATION NUMBER: US/09/731,030A
; PRIOR FILING DATE: 1997-12-29
; PRIOR APPLICATION NUMBER: 60/070,184
; NUMBER OF SEQ ID NOS: 21
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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 1343
; TYPE: DNA
; ORGANISM: Rattus sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2)..(673)
; OTHER INFORMATION: "n" is residue 1325; "n" represents to C, T, G, or A
US-09-731-030A-20
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Query Match          37.9%; Score 437.8; DB 10; Length 1343;
Best Local Similarity 78.6%; Pred. No. 3.6e-73;
Matches 523; Conservative 0; Mismatches 142; Indels 0; Gaps 0;
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OY 480 CCGGCTCTACGGCTTCATCGGCTCTGCTGGCTGCTGGCCGGCTGCTGGGATCTGCC 539
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Db 1 CCGTGTGATGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCC 60
OY 540 TTTCGTGGGCTGGAACCTGCTGGCCCTTTGACCGCTGCTGACGCTTCCTGACCTTCCTCCCTCTA 599
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 CCGTGGGCTGGAACCTGCTGGCCCTTTGACCGCTGCTGACGCTTCCTGACCTTCCTCCCTCTA 120
OY 600 CTCACAGCCGCTACATCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 659
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 121 CTCACAGGCGCTATGCTGCTCTTTGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
OY 660 GGGGCTCTATGGGGGCTATCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 719
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 181 GAGGCTCTATGGGGGCTATCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
OY 720 AGCGGCGCCGCGCAAGGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 779
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 241 TCTGCGCGCGCGCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
OY 780 CCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 839
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 301 TGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
OY 840 CTGGGCGCGCGCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 899
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 361 CTGGGCGCGCGCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
OY 900 GGGGCTGCAAGCCGCTACATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 959
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Db 421 AGGCAATCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
OY 960 CTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1019
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Db 481 CTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
OY 1020 GGGCGTGAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1079
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Db 541 GATACACGAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
OY 1080 CTTCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1139
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Db 601 TTTCGAGCTGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
OY 1140 CGTGC 1144
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Db 661 CATGC 665
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RESULT 9
US-10-037-616-3
; Sequence 3, Application US/10037616
; Patent No. US20020123148A1
; GENERAL INFORMATION:
; APPLICANT: English, Denis
; APPLICANT: Kovacs, Richard J.
; APPLICANT: Rizzo, Maria T.
; APPLICANT: Silva, Daniel T.
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; TITLE OF INVENTION: Sphingolipid Compositions and Methods for Their Therapeutic Use
; FILE REFERENCE: 7042-119
; CURRENT APPLICATION NUMBER: US/10/037,616
; CURRENT FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/243,887
; PRIOR FILING DATE: 2000-10-27
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1137
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1137)
; OTHER INFORMATION:
US-10-037-616-3
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Query Match          22.2%; Score 256; DB 12; Length 1137;
Best Local Similarity 56.7%; Pred. No. 1.7e-39;
Matches 513; Conservative 0; Mismatches 385; Indels 6; Gaps 2;
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Db 60 GCATACACCACTCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 119
OY 141 GGGCGCTGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 200
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Db 120 GCTACACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 179
OY 201 GCTGCGCGCATACCAAGCCATGCGGCTGCGCGGCGCGGCGCGGCGCGGCGCGGCGCGGCGCGGCGCGGCG 260
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Db 180 TTGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 229
OY 261 CATACGCTGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 320
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Db 240 CCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 299
OY 321 GGGCGCGCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 380
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Db 300 CAAGAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 359
OY 381 CGCGCTGCGCGCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 440
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 360 GGGCGCTGCGCGCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 419
OY 441 GGTGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 500
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Db 420 GATCAAAATGAGGCGCTTA--CGAGCGCAACAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 476
OY 501 CCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 560
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 477 GATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 536
OY 561 GTGCGCTTTGACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 620
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Db 537 GACAAATCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 596
OY 621 CTGCGCTGATCTTCTGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 680
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Db 597 CTGATACAGCATCTTCAAGGCGCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 656
OY 681 CCGGCTGCTGCGGCGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 740
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Db 657 CTTCCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 716
OY 741 CGCGCTGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 800
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 717 GGCAGCTGCTGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 776
OY 801 CTTCGCGGCTGCTGCTGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 860
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 777 CTTCATCTCTTCCTCATTTGATG--TGGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 833
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; Sequence 2, Application US/09971228
; Patent No. US2002015512A1
; GENERAL INFORMATION:
; APPLICANT: Liao, X. Charlene
; APPLICANT: Masuda, Esteban
; APPLICANT: Chu, Peter
; APPLICANT: Pardo, Jorge
; APPLICANT: Li, Congfen
; APPLICANT: Zhao, Haoran
; APPLICANT: Jiang, Yingping
; APPLICANT: Rigel Pharmaceuticals, Incorporated
; TITLE OF INVENTION: Edg: Modulators of Lymphocyte Activation and Migration
; FILE REFERENCE: 021044-000310US
; CURRENT APPLICATION NUMBER: US/09/971,228
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/284,763
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1032
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: mutant #1, C-terminally truncated variant of
; OTHER INFORMATION: human endothelial differentiation G-protein
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (9)..(1031)
; OTHER INFORMATION: mutant #1 human EDG1
US-09-971-228-2

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Query Match      20.6%; Score 237.4; DB 9; Length 1032;
Best Local Similarity 55.7%; Pred. No. 4.7e-36;
Matches 554; Conservative 0; Mismatches 411; Indels 30; Gaps 4;

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OY 61 CACAGCGCGCTCATGTTCTGACATACACACCTGGCGCGCGCGCGGCGG 120
Db 69 AACTATGATATATGCTCGGATTACACATACAGGGAACCTGAATATCAGCGCGGAC 128
OY 121 CCGGAGATGGCGGCTGGGCGCTGGGCGGCTGGGCGCGCGCGCGCTGGT 180
Db 129 AAGGAGAACAGATTAACCTGACC---TCGGTGGTGTTCATTTCTGCTGCTTATC 185
OY 181 GTGCTGAGAACCTGCTGCTGGCGGCGCATACACAGCCACATGCGGTGCGAGCGTGG 240
Db 186 ATCTGAGGAAACATCTTGTGCTGTGACCATTTGGAAACCAAGAAATTCACCGAGCC 245
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Db 483 CGCGCTTCCTGCTATATGACGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 542

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Db 603 CACAAGCAGCTATATCTCTTGTGACACCGAGCTTTCATCTGCTGCTGCTGCTGCTGCTG 662
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OY 940 GTGTGACAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 974
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; Sequence 1, Application US/09971228
; Patent No. US2002015512A1
; GENERAL INFORMATION:

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; APPLICANT: Liao, X. Charlene
; APPLICANT: Masuda, Esteban
; APPLICANT: Chu, Peter
; APPLICANT: Pardo, Jorge
; APPLICANT: Li, Congfen
; APPLICANT: Zhao, Haoran
; APPLICANT: Jiang, Yingping
; APPLICANT: Rigel Pharmaceuticals, Incorporated
; TITLE OF INVENTION: Edg: Modulators of Lymphocyte Activation and Migration
; FILE REFERENCE: 021044-000310US
; CURRENT APPLICATION NUMBER: US/09/971,228
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/284,763
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1149
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: wild-type human endothelial differentiation
; OTHER INFORMATION: G-protein coupled receptor (GPCR) 1 (EDG1)
; NAME/KEY: CDS
; LOCATION: (1)..(1149)
; OTHER INFORMATION: wild type human EDG1
US-09-971-228-1

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Query Match      20.6%; Score 237.4; DB 9; Length 1149;
Best Local Similarity 55.7%; Pred. No. 4.8e-36;
Matches 554; Conservative 0; Mismatches 411; Indels 30; Gaps 4;
OY 1 ATGAACGCCACGGGACCCCGGTGGCCCGAGTCTGCAACACAGTGGCGCGCGG 60

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 13, 2002, 08:33:56 : Search time 2202 Seconds

(without alignments)
8494.908 Million cell updates/sec

Title: US-09-786-926-2

Perfect score: 1155
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Scoring table: IDENTITY_NUC

Gapop 10.0, Capext 1.0

Searched: 16154066 segs, 809774376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: em_estha:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
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11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estlum:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	775	67.1	886	9	AL560216
3	763.2	66.1	804	13	BI910894
4	739.2	64.0	793	12	BG744043
5	692.6	60.0	930	13	BI824604
6	679.4	58.8	1057	14	BM922943

C	7	642	55.6	642	13	BI908610	BI908610	60306721
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C	11	593.2	51.4	957	9	AL582021	AL582021	
C	12	560	48.5	1506	13	BM550147	BM550147	AGENCOURT
C	13	551	47.7	998	10	BB610504	BB610504	
C	14	495	42.9	725	13	BI762628	BI762628	603048185
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C	16	391	33.9	729	12	BG744713	BG744713	602722823
C	17	355.2	30.8	711	9	AL543781	AL543781	
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C	20	339	29.4	1202	13	BM922670	BM922670	AGENCOURT
C	21	321.6	27.8	352	13	BI908474	BI908474	603069235
C	22	317	27.4	347	13	BI905951	BI905951	603062827
C	23	317	27.4	352	13	BI834290	BI834290	603084309
C	24	312.8	27.1	355	13	BI907722	BI907722	60306509
C	25	309	26.8	783	13	BI906435	BI906435	603063448
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C	27	289.8	25.1	359	13	BI909499	BI909499	603071074
C	28	280.2	24.3	630	9	AL58682	AL58682	u01a04.r
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C	42	203.4	17.6	745	12	BF281109	BF281109	EST445700
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ALIGNMENTS

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DEFINITION LTI_NFL010_BC2 Homo sapiens cDNA clone CS0DL003YC21 5
ACCESSION AL560608
VERSION AL560608
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 907)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, web : www.genoscope.cns.fr.

FEATURES

Location/Qualifiers
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/clone="CS0DL003YC21"
/clone_11b="LTI_NFL010_BC2"
/sex="male"
/tissue-type="B cells from Burkitt lymphoma"
/note="Vector: pcMVSPORT 6; Site_1: NotI; 1st strand cDNA

Rockville, Maryland 20850, USA. Fax: (1) 301 610 8371.

BASE COUNT	105 a	327 c	299 g	176 t
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Query Match	Score	DB 9;	Length
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QY	75	TGTTCTGACACACACACACACCGGGCGGGCTGGCGGGCGGGCGGGCGGAGATATGGCCG	134
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QY	375	CTTACACCGCCCTGGAGCGCGCTCCACACTTACAGCTCTCTTACACGAGGGAGACCTTTG	434
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QY	495	CATGGGCTCTGCTGCTGCTGTGGCCGCGCTCTCTGGGGATGCTGCTTGTGAGGCTGAA	554
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QY	795	CCCAATCTTGGGGTGTGTGTGGCGGAGACTCTTTGGCTTCCACATCTTGGCGCCAGAGATA	854
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LOCUS	AL560216	INT_FL011_B01	Homo sapiens	CDNA	clone CS00G002YR22 5 prime
DEFINITION	mRNA sequence.				
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BASE COUNT	103 a	311 c	299 g	172 t	1 others
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Dp	122	CCGAGGAGATGGCCGGCCCTGGGGGGCCCTGGGGGGGCTGTGGGGGGCCGCAAGTCCCTGGTG	181
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QY	241	GTCCTACTATTTGCTGGTGAACATCAGCTGTGAGTACCTGTCTACGGGCGGGCCCTACCTG	300
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 VERSION BG744043.1 GI:14054696
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
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 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1 (bases 1 to 793)
 NIH-MGC http://mhc.nci.nih.gov/
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished (1999)
 JOURNAL
 COMMENT
 Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: Dr. Daniel McVicar, DBS/MCI
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: L1CMI688 row: n column: 06
 High quality sequence stop: 783.
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 EcoRI; cDNA made by oligo-dT priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGCACGAG(G). Library constructed by Ling Hong in the
 laboratory of Gerald M. Rubin (University of California,
 Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
 Superscript II RT (Life Technologies). Note: this is a
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 BASE COUNT 95 a 284 c 270 g 144 t
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 721 GCGGCGCGCGCGCAGAGCGCCGCGCTGCTGTAAGCGGTGCTGATGCTCT 770
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 ACCESSION B1824604
 VERSION B1824604.1 GI:15936154
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1 (bases 1 to 930)
 NIH-MGC http://mhc.nci.nih.gov/
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished (1999)
 JOURNAL
 COMMENT
 Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: L1AM11435 row: c column: 09
 High quality sequence stop: 773.
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Query Match      60.0%: Score 692.6; DB 13; Length 930;
Best Local Similarity 93.0%: Pred. No. 1.6e-112;
Matches 814; Conservative 0; Mismatches 49; Indels 12; Gaps 8;

OY      85 TACAACTCGGCGCGGCTGGCCGGGCGGCGGAGAGATGGCGGCTGGGGGCC 144
      1 TAAACACACTCGGCGCGGCTGGCGGCGGCGGAGAGATGGCGGCTGGGGGCC 60
OY      145 CTGCGGGGGCTGTGCTGGTGGCGGCGGCTGGTGGTGGTGGTGGTGGTGGTGG 204
      61 CTGCGGGGGCTGTGCTGGTGGCGGCGGCTGGTGGTGGTGGTGGTGGTGGTGG 120
OY      205 GGGGCGCATACAGCCACATAGCGGCTGGCGAGCGTGGTGGTGGTGGTGGTGGTGG 264
      121 GGGGCGCATACAGCCACATAGCGGCTGGCGAGCGTGGTGGTGGTGGTGGTGG 180
OY      265 AGCGTGAAGTACCTGTGCTACAGGCGCGGCGGCTTACCTGGCCAGCTGCTGCTGCGG 324
      181 AGCGTGAAGTACCTGTGCTACAGGCGCGGCGGCTTACCTGGCCAGCTGCTGCTGCGG 240
OY      325 CGACACTTCCGTGTGGGGCCC -GCCAGTGGTGGTGGTGGTGGTGGTGGTGGTGG 383
      241 CGACACTTCCGTGTGGGGCCCCTGCCAGTGGTGGTGGTGGTGGTGGTGGTGGTGG 300
OY      384 CCGAGCGCGCTCCACCTTCAGCTGCTCTTCACTGCAAGGAGAGCGCTTGGCCACATGGT 443
      301 CCGAGCGCGCTCCACCTTCAGCTGCTCTTCACTGCAAGGAGAGCGCTTGGCCACATGGT 360
OY      444 GCGGCGCGGTGGCGGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 503
      361 GCGGCGCGGTGGCGGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 420
OY      504 CTGCTGGCTGGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 563
      421 CTGCTGGCTGGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 480
OY      564 CGCCTTGGACCGCTGCTCCAGCGCTTGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 623
      481 CGCCTTGGACCGCTGCTCCAGCGCTTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 540
OY      624 CCGTGGTGAATCTTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 683
      541 CCGTGGTGAATCTTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 600
OY      684 CCGTGGTGAATCTTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 740
      601 CCGTGGTGAATCTTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 660
OY      741 CCGCTGTGTAAGAGCGGTGCTGATGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 799
      661 CCGCTGTGTAAGAGCGGTGCTGATGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 719
OY      800 TCTTGGGCGTGGTGGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 859
      720 TCTTGGGCGTGGTGGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 777
OY      860 GGGGCGATGAGATG--ATCTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 916
      778 GGGGCGATGAGATG--ATCTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 837
OY      917 TCTACTCTTTC--GCAGCAGGAGGAGTGGCAGAGC 950
      838 ACTATCTTTC--GCAGCAGGAGGAGTGGCAGAGC 872

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RESULT 6      1057 bp      mRNA      linear      EST 12-MAR-2002
BM922943      BM922943
LOCUS      AGENCOURT_6632184 NIH_MGC_118 Homo sapiens. cDNA clone IMAGE:5756876
DEFINITION 5', mRNA sequence.

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ACCESSION      BM922943
VERSION        BM922943.1
KEYWORDS      GI:19373322
SOURCE        human.
ORGANISM      Homo sapiens
               Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Eukaryota; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE      NIH-MGC http://mgi.nci.nih.gov/
               National Institutes of Health, Mammalian Gene Collection (MGC)
               1 (bases 1 to 1057)
AUTHORS      Unpublished (1999)
TITLE        Contact: Robert Strausberg, Ph.D.
               Email: cga@b.jrnl.nih.gov
COMMENT      Tissue Procurement: Life Technologies, Inc.
               CDNA Library Preparation: Life Technologies, Inc.
               CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
               DNA Sequencing by: Agencourt Bioscience Corporation
               Clone distribution: MGC clone distribution information can be
               found through the I.M.A.G.E. Consortium/LNL at:
               http://image.jnl.gov
               Plate: L1AM12798 row: c column: 21
               High quality sequence stop: 581.
               Location/Qualifiers
               1. 1057
               /organism="Homo sapiens"
               /db_xref="taxon:9606"
               /clone="IMAGE:5756876"
               /clone_1ib="NIH_MGC_118"
               /tissue_type="leukocyte"
               /lab_host="DH10B"
               /note="Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV
               (destroyed); RNA source leukocytes from anonymous pool of
               non-activated adult donors. Library is oligo-dr primed
               and directionally cloned (EcoRV site is destroyed upon
               cloning). Average insert size 1.7 kb, insert size range
               1.2-3.3 kb. Library is normalized and enriched for
               full-length clones and was constructed by C. Gruber
               (Invitrogen). Research Genetics tracking code 027. Note:
               this is a NIH_MGC Library."

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BASE COUNT      118 a      418 c      333 g      188 t
ORIGIN
Query Match      58.8%: Score 679.4; DB 14; Length 1057;
Best Local Similarity 91.0%: Pred. No. 3.5e-110;
Matches 793; Conservative 0; Mismatches 61; Indels 17; Gaps 6;

OY      1 ATGAAGGCCAGGCGGAGCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 60
      21 ATGAAGGCCAGGCGGAGCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 80
OY      61 CACAGCGCGCTCATTTGTTGCACTACAACTGCGGCGGCGGCGGCGGCGGCGGCGGCGG 120
      81 CACAGCGCGCTCATTTGTTGCACTACAACTGCGGCGGCGGCGGCGGCGGCGGCGGCGG 140
OY      121 CCGGAGATGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 180
      141 CCGGAGATGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 200
OY      181 GTGCTGAGAACTTGTGCTGCTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240
      201 GTGCTGAGAACTTGTGCTGCTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 260
OY      241 GTCTACTATTGCTGTGTAACATACAGCTAGTACTGCTGCAAGGCGGCGGCGGCGGCGG 300
      261 GTCTACTATTGCTGTGTAACATACAGCTAGTACTGCTGCAAGGCGGCGGCGGCGGCGG 320
OY      301 GCCAAGCGTGTGCTGTGGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 360
      321 GCCAAGCGTGTGCTGTGGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 380
OY      361 CGGAGAGGCGTGTCTTACCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 420
      381 CGGAGAGGCGTGTCTTACCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 440

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|||||
Db 529 CTGCTGGCCTTCCGTGTGTCTGTGGGCGCCACTCTTGGGCTGTGTGTGTGTGTGTGTGT 470
OY 829 GAGTCACACTCTGTGGGCGCCAGAGATCTGTGGGCGATGATGATCTGTGGCCTGTGGC 888
Db 469 GGCCTCAACCTCTGTGGGCGCCAGAGATG-CTGGGCGCATGTGATCTGTGGCCTGTGGC 411
OY 889 GTCTCAACTGTGGGCGCCAGAGATCTGTGGGCGATGATGATCTGTGGCCTGTGGC 948
Db 410 GTCTCAACTGTGGGCGCCAGAGATCTGTGGGCGATGATGATCTGTGGCCTGTGGC 351
OY 949 GCGCTGTACCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1008
Db 350 GCGCTGTACCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 291
OY 1009 TGCGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1068
Db 290 TGCGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 231
OY 1069 CCAAGGAGACACTTTCGCGCGCTCCCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1128
Db 230 CCAAGGAGACACTTTCGCGCGCTCCCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 171
OY 1129 AGCATCTCCAGCGTGGCGAGCATCTGA 1155
Db 170 AGCATCTCCAGCGTGGCGAGCATCTGA 144

RESULT 10
AL543816 707 bp mRNA linear EST 16-FEB-2001
LOCUS AL543816 LTI_NFL006_P12 Homo sapiens cDNA clone CS0D1005YA17 5
DEFINITION AL543816 LTI_NFL006_P12 Homo sapiens cDNA clone CS0D1005YA17 5
ACCESSION AL543816
VERSION AL543816.1 GI:12876295
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 707)
AUTHORS Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr,
Location/Qualifiers
1. 707
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0D1005YA17"
/clone_lib="LTI_NFL006_P12"
/tissue_type="Placenta"
/note="Vector: pCMVSPORT 6; Site: 1: NotI, 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
cloned, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies Contact: Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifestech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT 93 a 231 c 204 g 146 t 33 others
ORIGIN
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|||||
Db 1 CTGCAAAAGCTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 60
OY 96 GGGCGCGCTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 155
Db 61 GGGCGCGCTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 120
OY 156 GTGGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCA 211
Db 121 TTGGGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCA 180
OY 212 TGAC-CAGCCACATGTGGCTGTGGCGAGCGTGGGTCTACTATTGCTGTGTGTGTGTGT 270
Db 181 TCACCAACACATGTGGCTGTGGCGAGCGTGGGTCTACTATTGCTGTGTGTGTGTGTGT 240
OY 271 AGTACACTGTGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 330
Db 241 AGTACACTGTGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300
OY 331 TTGCGTGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 389
Db 301 TTGCGTGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360
OY 390 CGCTTCACCTTTCAGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 449
Db 361 CGCTTCACCTTTCAGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 420
OY 450 GGTGGCGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 509
Db 421 GGTGGCGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 480
OY 510 GGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 569
Db 481 GGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 540
OY 570 TGACCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 629
Db 541 TGACCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 600
OY 630 GATCTTCGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 689
Db 601 GATCTTCGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 660
OY 690 GAGGCGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAG 736
Db 661 GAGGCGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAG 707

RESULT 11
AL582021/c 957 bp mRNA linear EST 16-FEB-2001
LOCUS AL582021 LTI_NFL010_BC2 Homo sapiens cDNA clone CS0D1003YC21 3
DEFINITION AL582021 LTI_NFL010_BC2 Homo sapiens cDNA clone CS0D1003YC21 3
ACCESSION AL582021
VERSION AL582021.1 GI:12949597
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 957)
AUTHORS Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr,
Location/Qualifiers
1. 957
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0D1003YC21"
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/clone_lib="LTL_NFL010_BC2"
/sex="male"
/tissue_type="B cells from Burkitt lymphoma"
/notes="Vector: PCWSPORT 6; Site 1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the PCWSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@life.com url :
http://fulllength.invitrogen.com"
BASE COUNT      200 a      289 c      320 g      139 t      9 others
ORIGIN

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Query Match      51.4%; Score 593.2; DB 9; Length 957;
Best Local Similarity 99.4%; Pred. No. 5.4e-95;
Matches 614; Conservative 2; Mismatches 0; Indels 2; Gaps 2;

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OY 538 CTTTGTGGGCTGGAACGCTGTGGGCTTTGACCGGTGTCAGCCTTGTGCCCCC 597
DB 956 CTTTGTGGGCTGGAACGCTGTGGGCTTTGACCGGTGTCAGCCTTGTGCCCCC 897
OY 598 TACTCCAAAGCCCTACATCTCTTGTGCTGTGATTTTGGCGGTCTGTGACACATC 657
DB 896 TACTCCAAAGCCCTACATCTCTTGTGCTGTGATTTTGGCGGTCTGTGACACATC 837
OY 658 ATGGGCTCTATGGGCTATCTTCCGCTGTGTCAGAGCCAGAGGAGGAGGAGGAGG 717
DB 836 ATGGGCTCTATGGGCTATCTTCCGCTGTGTCAGAGGAGGAGGAGGAGGAGGAGG 777
OY 718 CCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 777
DB 776 CCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 717
OY 778 TTCTGCTGTGCTGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 837
DB 716 TTCTGCTGTGCTGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 657
OY 838 CTCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 897
DB 656 CTCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 598
OY 898 TCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 957
DB 597 TCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 538
OY 958 AGCTTCTCTGTGCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1017
DB 537 AGCTTCTCTGTGCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 478
OY 1018 CGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1077
DB 477 CGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 418
OY 1078 AGCTTCTCTGTGCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1137
DB 417 A-STTTCCGGGCTCCCGGTGCTCAGCTTTGGATGCGGAGAGCCCTGTGCAGCATCTCC 359
OY 1138 AGCGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1155
DB 358 AGCGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 341

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RESULT 12
BM550147      1506 bp      mRNA      linear      EST 20-FEB-2002
LOCUS      AGNCOURT 6544010 NIH_MGC_118 Homo sapiens cDNA IMAGE:5746020
DEFINITION      5' mRNA sequence.
ACCESSION      BM550147
VERSION      BM550147.1 GI:18786109
KEYWORDS      EST.

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SOURCE
ORGANISM      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 1506)
AUTHORS      NIH-MGC http://mgl.ncl.nih.gov/.
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cga@rsf@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLM12769 row: 0 column: 13
High quality sequence stop: 511.
Location/Qualifiers
1. 1506
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5746020"
/clone_lib="NIH_MGC_118"
/tissue_type="Leukocyte"
/lab_host="DH10B"
/notes="Vector: PCW-SPORT6; Site 1: NotI; Site 2: EcoRV
(destroyed); RNA source leukocytes from anonymous pool of
non-activated adult donors. Library is oligo-dT primed
and directionally cloned. (EcoRV site is inserted upon
cloning). Average insert size 1.7 kb, insert size range
1.2-3.3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 027. Note:
this is a NIH_MGC Library."
BASE COUNT      188 a      586 c      433 g      297 t      2 others
ORIGIN

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Query Match      48.5%; Score 560; DB 13; Length 1506;
Best Local Similarity 97.1%; Pred. No. 4.2e-89;
Matches 602; Conservative 0; Mismatches 15; Indels 3; Gaps 3;

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OY 43 CAGCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 102
DB 1 CAGCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 60
OY 103 CTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 162
DB 61 CTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 120
OY 163 GCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 222
DB 121 GCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 180
OY 223 ATGCGGTGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 282
DB 181 ATGCGGTGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 240
OY 283 AGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 342
DB 241 AGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 300
OY 343 CCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 402
DB 301 CCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 360
OY 403 AGCTGCTCTTACATGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 462
DB 361 AGCTGCTCTTACATGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 420
OY 463 GGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 522

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DB	421	GGGCCACACAGACACACCGCGCTTACAGGCTTACATGGCCCTTCTGCTGGCTGTGGCCGCG	480
QY	523	CTCTGGGGAGTCGTG-CCTTTGCTGGGCTGTGAATGTCCTGTGGCGCTTTTGACCGCTGCTC	581
DB	481	CTGTGTGGGGATGTCTGGCCCTTTTCTGTGGGCTGGAGACCTGTGGCCCTTTTGACCGCTGCTC	540
QY	582	CAGCCTTCTGCCCCCTTACTACCAAGCG-CCTACATCTCTTCTG-CCTGGAGATCTTTCGCC	639
DB	541	CAACCTCTGCTGCCCCCTTACTACCAAGGCGCTACATCTTCTTGTGGCCTTGGGGATCTTCCCC	600
QY	640	GGCCTCTGTGGCCACATCAT 659	
DB	601	CGCGCTCTCTGGGCGCACAT 620	
RESULT 13			
LOCUS	BB610504		
DEFINITION	BB610504 RIKEN full-length enriched, adult male stomach Mus		
ACCESSION	BB610504		
VERSION	BB610504.1		
KEYWORDS	EST.		
ORGANISM	house mouse.		
SOURCE	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 998)		
AUTHORS	Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Itoh,M., Koyama,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,H., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toyota,T., Muramatsu,M. and Hayashizaki,Y. RIKEN Mouse ESTs (Arakawa,T., et al. 2001) Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222 Fax: 81-45-503-9216 Email: genome.res@sc.riken.go.jp/ URL: http://genome.gsc.riken.go.jp/ Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Kono,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000) wagui,K., Fujiwara,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Wataniki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsunura,S., Kawai,Y., Okazaki,Y., Muramatsu,M., Inoue,Y., Kita,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1571-1771 (2000) Kono,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y. Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanka,I., Aizawa,K., K., Fukuda,S., Hara,A., Itoh,M., Kawai,Y., Shibata,K. and Hayashizaki,Y. Computational Analysis of Full-length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details. e mouse tissues. Location/Qualifiers 1..998		
FEATURES			
source			

	Query Match	Best Local Similarity	Mismatches	709;	Conservative	47.7%; Score 551; DB 10; Length 998;	78.9%; Pred. No. 1,5e-87;	0; Mismatches 180; Indels 9; Gaps 4;
Y	1	ATGACGCCACGCGGAGCCCGGTGGCCCGGAGCTCCGACATCAAGTGGCGCGCGGGG 60						
Db	24	ATCAGTACTGTGTCCACGCTGTGTGCCCAAGTCTGCGACCGGCTGGCAGCAGCGGC 83						
Y	61	CACAGCGGCTCATTTTCTGCATCAACCACTCGGGCGGCTGGCCCGGGGG 120						
Db	84	CACAGCCTCTCATTTTCTGCATCAACCACTCGGGCGGCTGGCCCGGGGG 143						
Y	121	CCGAGGA--TGGCGGCTGGGGGCGCTGGGGGGGTGGTGGTGGCCCAAGTGGCTG 177						
Db	144	TCGAGGACGCTGAGAGGCTAGGATGTCTGAGGGGGCGTGGTGGCG-CAGTTGGCTG 202						
Y	178	GTGGTGTGGAGAACTGTGTGGTGGCGGGCCATCAACGACCAATGGGGTGGGAGAGC 237						
Db	203	GTGGTGTGGAGAACTGTGTGGTGGCGGGCCATCAACGACCAATGGGGTGGGAGAGC 262						
Y	238	TGGGTCTACTATTGCTGGTGAATCACTGCTGAAGTACCTGCTCAAGCGCGGCTTAC 297						
Db	263	TGGGTCTACTATTGCTGGTGAATCACTGCTGAAGTACCTGCTCAAGCGCGGCTTAC 322						
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AUTHORS			
NIH-MGC http://mgc.nci.nih.gov/ .			
TITLE			
National Institutes of Health, Mammalian Gene Collection (MGC)			
JOURNAL			
Unpublished (1999)			
COMMENT			
Contact: Robert Strausberg, Ph.D.			
Email: cgabbs@email.nih.gov			
Tissue Procurement: Life Technologies, Inc.			
cDNA Library Preparation: Life Technologies, Inc.			
DNA Sequencing by: Incyte Genomics, Inc.			
Clone distribution: MGC clone distribution information can be			
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female, 71 yo male colon; 46 yo male kidney, and pool of 2			
stomachs, 62 yo male and 70 yo female. Library is			
oligo-dr primed and directionally cloned (EcoRV site is			
destroyed upon cloning). Average insert size 1.4 kb,			
insert size range 1-3 kb. Library is normalized and			
enriched for full-length clones and was constructed by C.			
Gruber (Invitrogen). Research Genetics tracking code			
023. Note: this is a NIH.MGC library."			
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ORIGIN			
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Accession	Source	Organism	Reference	Authors	Title	Journal	Comment
709	GenBank	Mus musculus	768	Zhao, S., Nierman, W., Malek, J., Shatsman, S., Akhmet, B., Levins, M., Tsegaye, G., Geer, K., Kroll, M., Shvartsbeyn, A., Gebreyes, E., Russell, D., de Jong, P., and Fraser, C. M.	Mouse BAC End Sequences from Library RPCI-24	Unpublished (1999)	Other GSSs: RPCI-24-120122.TV
769	GenBank	Mus musculus	828	Shao, Y., Zhao, S., Nierman, W., Malek, J., Shatsman, S., Akhmet, B., Levins, M., Tsegaye, G., Geer, K., Kroll, M., Shvartsbeyn, A., Gebreyes, E., Russell, D., de Jong, P., and Fraser, C. M.	Mouse BAC End Sequences from Library RPCI-24	Unpublished (1999)	Other GSSs: RPCI-24-120122.TV
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889	GenBank	Mus musculus	948	Shao, Y., Zhao, S., Nierman, W., Malek, J., Shatsman, S., Akhmet, B., Levins, M., Tsegaye, G., Geer, K., Kroll, M., Shvartsbeyn, A., Gebreyes, E., Russell, D., de Jong, P., and Fraser, C. M.	Mouse BAC End Sequences from Library RPCI-24	Unpublished (1999)	Other GSSs: RPCI-24-120122.TV
240	GenBank	Mus musculus	299	Shao, Y., Zhao, S., Nierman, W., Malek, J., Shatsman, S., Akhmet, B., Levins, M., Tsegaye, G., Geer, K., Kroll, M., Shvartsbeyn, A., Gebreyes, E., Russell, D., de Jong, P., and Fraser, C. M.	Mouse BAC End Sequences from Library RPCI-24	Unpublished (1999)	Other GSSs: RPCI-24-120122.TV
949	GenBank	Mus musculus	1008	Shao, Y., Zhao, S., Nierman, W., Malek, J., Shatsman, S., Akhmet, B., Levins, M., Tsegaye, G., Geer, K., Kroll, M., Shvartsbeyn, A., Gebreyes, E., Russell, D., de Jong, P., and Fraser, C. M.	Mouse BAC End Sequences from Library RPCI-24	Unpublished (1999)	Other GSSs: RPCI-24-120122.TV
300	GenBank	Mus musculus	359	Shao, Y., Zhao, S., Nierman, W., Malek, J., Shatsman, S., Akhmet, B., Levins, M., Tsegaye, G., Geer, K., Kroll, M., Shvartsbeyn, A., Gebreyes, E., Russell, D., de Jong, P., and Fraser, C. M.	Mouse BAC End Sequences from Library RPCI-24	Unpublished (1999)	Other GSSs: RPCI-24-120122.TV
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360	GenBank	Mus musculus	419	Shao, Y., Zhao, S., Nierman, W., Malek, J., Shatsman, S., Akhmet, B., Levins, M., Tsegaye, G., Geer, K., Kroll, M., Shvartsbeyn, A., Gebreyes, E., Russell, D., de Jong, P., and Fraser, C. M.	Mouse BAC End Sequences from Library RPCI-24	Unpublished (1999)	Other GSSs: RPCI-24-120122.TV
1069	GenBank	Mus musculus	1128	Shao, Y., Zhao, S., Nierman, W., Malek, J., Shatsman, S., Akhmet, B., Levins, M., Tsegaye, G., Geer, K., Kroll, M., Shvartsbeyn, A., Gebreyes, E., Russell, D., de Jong, P., and Fraser, C. M.	Mouse BAC End Sequences from Library RPCI-24	Unpublished (1999)	Other GSSs: RPCI-24-120122.TV
420	GenBank	Mus musculus	479	Shao, Y., Zhao, S., Nierman, W., Malek, J., Shatsman, S., Akhmet, B., Levins, M., Tsegaye, G., Geer, K., Kroll, M., Shvartsbeyn, A., Gebreyes, E., Russell, D., de Jong, P., and Fraser, C. M.	Mouse BAC End Sequences from Library RPCI-24	Unpublished (1999)	Other GSSs: RPCI-24-120122.TV
1129	GenBank	Mus musculus	1155	Shao, Y., Zhao, S., Nierman, W., Malek, J., Shatsman, S., Akhmet, B., Levins, M., Tsegaye, G., Geer, K., Kroll, M., Shvartsbeyn, A., Gebreyes, E., Russell, D., de Jong, P., and Fraser, C. M.	Mouse BAC End Sequences from Library RPCI-24	Unpublished (1999)	Other GSSs: RPCI-24-120122.TV
480	GenBank	Mus musculus	506	Shao, Y., Zhao, S., Nierman, W., Malek, J., Shatsman, S., Akhmet, B., Levins, M., Tsegaye, G., Geer, K., Kroll, M., Shvartsbeyn, A., Gebreyes, E., Russell, D., de Jong, P., and Fraser, C. M.	Mouse BAC End Sequences from Library RPCI-24	Unpublished (1999)	Other GSSs: RPCI-24-120122.TV
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AUTHORS							
TITLE							
JOURNAL							
COMMENT							

GenCore version 5.1.3
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Run on: December 13, 2002, 08:37:36 ; Search time 75 Seconds
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

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ALIGNMENTS

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; Patent No. 6060272
; GENERAL INFORMATION:
; APPLICANT: Li et al.
; TITLE OF INVENTION: Human G-Protein Coupled Receptors
; FILE REFERENCE: 1488.1220000
; CURRENT APPLICATION NUMBER: US/08/852.824C
; CURRENT FILING DATE: 1997-05-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1637
; TYPE: DNA
; ORGANISM: genomic
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (50)..(1201)
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RESULT 2
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; Sequence 2, Application US/0845566
; Patent No. 5912144
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice
; APPLICANT: Guegler, Karl
; TITLE OF INVENTION: EDG-1 LIKE RECEPTOR
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:

Query Match 95.7% Score 1104.8; DB 2: Length 1649;
Best Local Similarity 99.2%; Pred. No. 1.5e-199;
Matches 1150; Conservative 0; Mismatches 5; Indels 4; Gaps 4;
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/845,566
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0271 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0595
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1649 base pairs
TYPE: nucleic acid
STRADEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: TYNMOR01
CLONE: 144690
US-08-845-566-2

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Db	610	TCCAAGGCGATACATCCTTCTGCGCTGAGATCTTGGCGGCGTCCAGGCGCATCATG	669
Qy	661	GGCCTCATGAGGCGCATCTTCCGCTGCTGTCAGAGCCAGCGGCGAGAAGGCCACAGCCCA	720
Db	670	GGCCTCATGAGGCGCATCTTCCGCTGCTGTCAGAGCCAGCGGCGAGAAGGCCACAGCCCA	729
Qy	721	GGCGCCCGCGCAAGGCGCGCCGCTGCTGAGAGAGCGGTCTATGATCCGTGGGCTTC	780
Db	730	GGCGCCCGCGCGCAAGGCGCGCCGCTGCTGAGAGAGCGGTCTATGATCCGTGGGCTTC	789
Qy	781	CTGCTGTGCTGAGGCGCCACCTTTC-6GGCTGCTGCTGAGCCAGCGTCTTTGGCTCCAACT	839
Db	790	CTGCTGTGCTGAGGCGCCACCTTTCGCGGCGCTGCTGCTGCGCCAGCGTCTTTGGCTCCAACT	849
Qy	840	CTGGGGCCCAAGAGTACCTGCGGGGCGATGAGATCCTGCGCCGCGCTCCTCAACT	899
Db	850	CTGGGGCCCAAGAGTACCTGCGGGGCGATGAGATCCTGCGCCGCGCTCCTCAACT	909
Qy	900	GGCGGTCAACCCCATCATCTACTACTCTTCCGACAGGAGGAGTGTGTCAGAGCCGTGCTCAG	959
Db	910	GGCGGTCAACCCCATCATCTACTACTCTTCCGACAGGAGGAGTGTGTCAGAGCCGTGCTCAG	969
Qy	960	-CTTCTCTCTGCTGCGGCTGTCTCCGCGCTGAGCATGCGAGGCGCC-6GGGATGCTCTGGCC	1017
Db	970	CTTCTCTCTGCTGCGGCTGTCTCCGCGCTGAGCATGCGAGGCGCCGAGGCGGAGTCTGCGCC	1029
Qy	1018	CGGCGCCCTCAGAGGCTCACTCCGAGGCTTCC-ACCACCGACAGCTCTGTAGGCGCAAGGGA	1076
Db	1030	CGGCGCCCTCAGAGGCTCACTCCGAGGCTTCCACACCGACAGCTCTGTAGGCGCAAGGGA	1088
Qy	1077	CAGCTTTCGCGGCTCCCGCTCGCTCAAGCTTTCGGATGCGGAGCCCTGTCTCAGCATCTC	1138
Db	1090	CAGCTTTCGCGGCTCCCGCTCGCTCGCTCAGCTTTCGGATGCGGAGCCCTGTCTCAGCATCTC	1149
Qy -	1137	CAGCGTGGGAGCATCTGA 1155	
Db	1150	CAGCGTGGGAGCATCTGA 1168	
<p>RESULT 3</p> <p>US-09-082-088-1</p> <p>Sequence 1, Application US/09082088</p> <p>Patent No. 6130067</p> <p>GENERAL INFORMATION:</p> <p>APPLICANT: TSUI, PING</p> <p>TITLE OF INVENTION: HUMAN EDG3sb GENE</p> <p>NUMBER OF SEQUENCES: 2</p> <p>CORRESPONDENCE ADDRESS:</p> <p>ADDRESSEE: Ratner & Prestlia</p> <p>STREET: P.O. Box 980</p> <p>CITY: Valley Forge</p> <p>STATE: PA</p> <p>COUNTRY: USA</p> <p>ZIP: 19482</p> <p>COMPUTER READABLE FORM:</p> <p>MEDIUM TYPE: Diskette</p> <p>COMPUTER: IBM Compatible</p> <p>OPERATING SYSTEM: DOS</p> <p>SOFTWARE: FastSeq for Windows Version 2.0</p> <p>CURRENT APPLICATION DATA:</p> <p>APPLICATION NUMBER: US/09/082,088</p> <p>FILING DATE: 20-MAY-1998</p> <p>CLASSIFICATION:</p> <p>PRIOR APPLICATION DATA:</p> <p>APPLICATION NUMBER:</p> <p>FILING DATE:</p> <p>ATTORNEY/AGENT INFORMATION:</p> <p>NAME: Prestlia, Paul F</p> <p>REGISTRATION NUMBER: 23,031</p> <p>REFERENCE/DOCKET NUMBER: GP-70453</p> <p>TELECOMMUNICATION INFORMATION:</p> <p>TELEPHONE: 610-407-0700</p>			

	TELEFX: 610-407-0701	TELEX:	INFORMATION FOR SEQ. ID NO: 1:	SEQUENCE CHARACTERISTICS:	LENGTH: 1137 base pairs	type: nucleic acid	STRANDEDNESS: single	TOPOLOGY: linear	MOLECULE TYPE: cDNA	US-09-082-088-1
Query Match	22.0%; Score 254.4; DB 3; Length 1137;									
Best Local Similarity	56.6%;	Pred. NO. 8.3e-40;								
Matches 512;	Conservative 0;	Mismatches 386;	Indels 6;	Gaps 2						
QY	81	GCATTAACCACTCGGGCGGCTGGCCGGGGCGGGGGCCGGAGATGGCGGCTGGG	140							
Db	60	GCATTACCACTACGTGGGGAGATTGGCGGGGAGGCTGAAGAGAGCCCTCCGAGGCGACAC	119							
QY	141	GGCCCTCGGGGGGCTGCGGTGGCCGCCACAGCTGCCTGGTGGTGGAGAACTTGCTGT	200							
Db	120	GCTACACACGCTGCTCTTCTGGTATCTGACGACTTCACTGCTTTGGAGAACCTGATGCT	179							
QY	201	GCTGGCGCCATCAACAGCCACATGCGGGTGCAGCGCTGGCTTACTATTGCTGTGA	260							
Db	180	TTTATTATTCTTGGAATAATTAATTCACAACCGCATGACTTTTTCATTGGCA	239							
QY	261	CATACGCTGATGACCTGCTACAGGGGCGGCGCTACCTGGGCAACGCGCTGCTGGG	320							
Db	240	CTTGCTCTCTGAGACTGCTGGCGCGGCACTGCTTACAAAGTCAACATTTGATGCTGG	299							
QY	321	GGCCCGACCTTCGCTGGCGCCGCCACAGTGTTCTTACGGGAGGCGCTGCTTTAC	380							
Db	300	CAGAAACGCTGACGCTGCTGCCACGGCTGCTTCCACAGGAGGAGCAATGTTGCT	359							
QY	381	CGCCCTGGCGGCTCTCACCTTACGCTGCTTCTTCACTGACAGGAGAGCGCTTGGCACAT	440							
Db	360	GGCCCTGGGGGCGTCACTCGACGTTACTGGCTTCATGCACTGACGAGCGCACTTGACAT	419							
QY	441	GGTCGGGCGGTGGCGAGAGCGGGGCGACAAAGACCAAGCGCGCTTACGCTTACATCGG	500							
Db	420	GATCAAAATGAGGCGCTTA---CGAGCGCAAAAGAGGACCGCGCTTCCCTCGATCGG	476							
QY	501	CCTGCTGGCTGCTGGCGCGCTGCTGGGGGATGCTGCCCTTTCCTGGGCTTGAATGCTCT	560							
Db	477	GATGTGCTGCTATTGCTTCACGCTGGCGCCCTCGCCATTCCTGGGCTGGAATGCTCT	536							
QY	561	GTCGGCCTTTCAGCGCGTGCACGACCTTTCGCGCCCTTACATGCAAGGCGTCACTCTCT	620							
Db	537	GCAAAATCTCCGAGCTGCTTACATCTGAGCCCTCTACTCTCAAGAAATGATCATTTGCTT	596							
QY	621	CTGCGCTGATATCTTGCGCGGCGCTGCTGGCCACATCATGGCGCTTATGGGGCATCTT	680							
Db	597	CTGCATCAGATCTTTCACGGCCATCTCTGCTGACATCTGATCTCTACGACCATCTTA	656							
QY	681	CGCGCTGTGTGAGGCGAGGGGAGAGGCCGCCACGCGGCGCGCGCGGCGGCAAGGGCCG	740							
Db	657	CTTCTGTGTGAAGTCAGACGCCGTAAAGTGGCAACCAACAAACATCTGGAGCGTCCAT	716							
QY	741	CCGCGCTGTGAAGCGGTGCTGATGATCTCTGCTGGCGTCTCTGATGCTGGGGCCACT	800							
Db	717	GGCACTGTGTGGACCGTGTGATTTGTGTGAGCGGTTCATCGGCTCTGCTGTGCCACT	776							
QY	801	CTTGCGGCTGCTGTGGCGGACGCTCTTTGGCTTCAACCTCTGGGCGGAGAGTACCTGGC	860							
Db	777	CTTCATCTCTCTCTCATTTGATG---TGCGCTGACGGGTGACGGGTGCTCCCATCTCTT	833							
QY	861	GGGCGATGAGATCTTGCGCTGCGCGCTTCAACTGAGCGGAGCAACCCCATCATCTTA	920							
Db	834	CAAGGCTCAGTGTGATGCTGTGGCTGTGCTCAACTTCGCGCATGAAACCGGCTCATCTTA	893							
QY	921	CTGCTTCCGAGCAGGAGGCTGTGAGAGCCGCTGCTCAAGCTTCTCTGCTGCGGGTCTCT	980							

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Db 894 CAGCGTGGCCAGCAAGAGATGCGGGGCGCTTCTTCGCTGTGTGCAACTGCGTGGT 953
QY 981 CCGG 984
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Db 954 CAGG 957

RESULT 4
; Sequence 1, Application US/09546117
; Patent No. 6344542
; GENERAL INFORMATION:
; APPLICANT: TSUI, PING
; TITLE OF INVENTION: HUMAN EDG3sb GENE
; FILE REFERENCE: GP-70453-D1
; CURRENT APPLICATION NUMBER: US/09/546,117
; PRIOR FILING DATE: 1998-05-20
; PRIOR APPLICATION NUMBER: 09/082,088
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1137
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
US-09-546-117-1

Query Match      22.0%; Score 254.4; DB 4; Length 1137;
Best Local Similarity 56.6%; Pred. No. 8.3e-40;
Matches 512; Conservative 0; Mismatches 386; Indels 6; Gaps 2;

QY 81 GCACCTACCAACCACTCGGGCGCGGCGCGCGCGCGCGCGCGAGATGGCGGCGCTGGG 140
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 60 GCATTACCAAGTACGTGGGGAAGTTGGCGGAGCGCTGAAGAGAGCGCTCCGAGGCGAGAC 119
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 141 GGCCTGGGGGGGCTGTGGTGGCCGACGCTGCTGTGTGTGCTGGGAACCTGTGTGT 200
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 120 GCTCACCAACCGGCTCTTCTGTGTGTATGTGACGCTTCACTCTTGTAGGAACCTGTATGT 179
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 201 GCTGGCGGACATCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 260
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 180 TTTGATTCGCACTGTGAAAACAATAAATTTCACACGCGCATGACTTTTCATTTGCGAA 239
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 261 CATCACGCTGATGACCTGCTCAGCGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 320
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 240 CTTGCTCTCTGCGACCTGCTGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 299
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 321 GGGCGGCGACCTCGCTGGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 380
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 300 CAGAAGAGAGCTTACGCTGTCTCCACGCGTGTGCTCTCAAGGAGGCGAGATGTTCTGT 359
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 381 CGCCCTGGCGCGCTTACGCTTACGCTTCTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 440
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 360 GGGCGCTTGGGGGCTCAGCTGTGAGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 419
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 441 GGTGGCGCGGCTGGCGGAGAGCGGGGCGCAACAAGACCGCGCTCTAAGGCTTCTATCGG 500
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 420 GATCAAAATGAGGCCCTTA---CGAGGCCAACAAGAGGCGCGCTCTCTCTCTCTCTCTCT 476
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 501 CCGTGGCGGCTGTGGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 560
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 477 GATGTGTGGCTCATGTGCTTACGCTGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 536
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 561 GTGGCGCTTTGACGCGCTTCCAGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 620
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 537 GCACAAATCTCCCTGACTCTCTACATCTCTGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 596
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 621 CTGGCTGTGATCTTCTGGCGGCGGCTCTGGCGCAACATATGCGGCTCTATGCGGCGCATCTT 680
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 597 TTTGCTATGAGCATCTTCAAGCGGCATCTGTGTGACCATCTGTATCTCTTACGACGACATCTA 656
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 681 CCGCTGTGTGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 740
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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Db 657 CTTCCTGTGTAAGTCCAGCAGCCGTAAGTGTGCCAACACMACACTCGGAGCGGTTCAT 716
QY 741 CCGCTGTGTAAGAGCGGTGTGTGATTCCTGCTGGCGCTTCTCTGTGTGGGGGCCACT 800
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 717 GGCACCTCTCGGACCGCTGTGTGATTTGGTAGCGGTGTTCATGCTGCTGCTGCCACT 776
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 801 CTTCGGGCTCTGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 860
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 777 CTTCATCTCTTCCTCATATGATG---TGCGCTCAGGGGTGACAGCGGTGCCCATCTCTT 833
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 861 GGGCATGAGTGAATCTGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 920
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 834 CAAGGCTCAGTGTTCATCTGTGGCTGTGCTCAACTCGGCGCATGACCCGCTCATCTA 893
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 921 CTCCTTCGAGGAGGAGGTGTGACAGCGCGGCTCAGCGCTCTGCTGCTGGGGGTGTCT 980
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 894 CAGCGTGGCCAGCAAGAGATGCGGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 953
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 981 CCGG 984
   ||
Db 954 CAGG 957

RESULT 5
US-09-262-477-1
; Sequence 1, Application US/09262477A
; Patent No. 6423508
; GENERAL INFORMATION:
; APPLICANT: George Liyi
; APPLICANT: Derek Bergsma
; APPLICANT: Jeffrey Stadel
; APPLICANT: Winnie Chan
; APPLICANT: Shelaigh Johnson
; APPLICANT: Jon Chambers
; APPLICANT: Phillip Robert
; APPLICANT: Nasirah Khandoudi
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDE SEQUENCES OF HUMAN EDG-1C AND
; TITLE OF INVENTION: METHODS OF SCREENING FOR AGONISTS AND ANTAGONISTS FOR HUMAN
; TITLE OF INVENTION: EDG-1C RECEPTOR AND SPHINGOSINE 1-PHOSPHATE LIGAND AND
; FILE REFERENCE: GP50006
; CURRENT APPLICATION NUMBER: US/09/262,477A
; EARLIER FILING DATE: 1999-03-04
; EARLIER APPLICATION NUMBER: 60/077,369
; EARLIER FILING DATE: 1998-03-09
; EARLIER APPLICATION NUMBER: 60/087,102
; EARLIER FILING DATE: 1998-05-28
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1149
; TYPE: DNA
; ORGANISM: Human
US-09-262-477-1

Query Match      20.6%; Score 237.4; DB 4; Length 1149;
Best Local Similarity 55.7%; Pred. No. 1.3e-36;
Matches 554; Conservative 0; Mismatches 411; Indels 30; Gaps 4;

QY 1 ATGAGCGCCACGCGGAGCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 60
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 ATGGGGCGCCACGCGCTCCCGCTGCTCAAGGCCACCGAGCTCGGCTCTCTACTACTATCTC 60
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 61 CACAGCGGCTCTATGTGTGCACTAACAACACTGGGGCGGCTGGCGGGCGGGGGGGG 120
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 AACTATGATATCATGCGCGGCACTTACACTACGCGGGAAGCTGATATACAGCGGGGAGC 120
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 121 CCGAGAGATGCGGCGGCTGGGGCGGCTGGCGGGGCTGTGCGGCGGCGGCGGCGGCGGCGG 180
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 121 AAGGAGACAGCATTAACATGACC---TGGGTGTGTTCATTTCTATCTATGCTGCTTTATC 177
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 181 GTGCTGGAGAACTTGTGTGTGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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178 ATCTGAGAGACATCTTGTCTGTGACCATTTGGAAAACCAAGAAATTCACACGCC 237
241 GTCCTACTTTCCTGCGTGAACATCAGCTGAGTACGCTGTCACGGGGCGGCTTAC 300
238 ATGTCTATTATTATTGCAATCTGGCCCTCTCAGACTCTGTGGCAGAGTAGTACCA 237
301 GCCAAGCTGTGCTGTGCGGGGGCCGACCTTCCTGTGGCGCCCGCCAGTGTCTTA 360
298 GCTAACCTGCTCTGTCTGGGGCCACCACTACAGCTACCTCCGCGCCAGTGGTCTG 357
361 CGGAGGCGCTGTCTCTACCGCCCTGCGCCCTCAGCTTCCAGCTTCCAGCTTCA 420
358 CGGAGAGGAGATATGTTTGTGGCCCTGTACGCTCCGCTTCAAGTCTCTCTGCA 417
421 GGGAGCGCTTGTGCGCATGTGCGCGCGGTGGCCGAGAGCGGGGCCACCAAGCAG 480
418 ATTGAGCGCTTATACAAATGCTGAAATGAAATCCAAACGAGG--AGCAATACCT 474
481 CGCGCTAGCGCTTCAATCGGCTCTGTGCTGCTGCGCGCGCTGCTGCGGATGCT 540
475 CGGCTCTCTCTGTAATCAGCGCGCTGTGGGTCACTCTCTCATCTGGTGGCTGCT 534
541 TTGCTGGCGCTGGAGCTGCTGTGCGCTTGTGACCGCTGTCTCAGCTTCTGCTCT 600
535 ATCATGAGGCTGGAACCTCATCATGCGCTGTCTCAGCTGTCTCAGCTGTGCGCT 594
601 TCCAAAGCGCTACATCTCTCTCTGCTGTGATCTTCCGCGCGCTCTGCGCACAT 660
595 CACAAGCACTATCTCTCTCTCTCTGACACGCGCTTCTCTCTCTCTCTCTCTCT 654
661 GCGCTCTCTGCGGCGCTCTCTCTGCTGTGATGCGCGCGCGCGCGCGCGCGCG 720
655 ATTCTGTACTGCAATCTCTCTCTGTGTGTGAGACTGAGAGCGCGCGCTCTCT 714
721 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 759
715 AAGAACTATTCACAAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 774
760 CTGATGATCTGCTGCTGCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 819
775 ATTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 834
820 GACGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 879
835 GATG--TGGGCTGCAAGCTGTAAGACCTGTGACATCTCTTCAAGCGGAGTCT 891
880 GCGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 939
892 GTGTTAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 951
940 GTGTGAGAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 974
952 ATGCGTGGCGCTTATCTGCGGATGATGCTGCTGCTGCTGCTGCTGCTGCTG 986

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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/196, 989B
FILING DATE: 15-FEB-1994
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Lloyd, Jeff
REGISTRATION NUMBER: 35,589
REFERENCE/DOCKET NUMBER: MAC-100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2232 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 269..1420
US-08-196-989B-3

Query Match          19.94; Score 230.2; DB 1; Length 2232;
Best Local Similarity 55.3%; Pred. No. 3, 1e-35;
Matches 548; Conservative 0; Mismatches 413; Indels 30; Gaps 4;

2 TGAAGCCGACGGGAGACCCCGGGGCGCCCGAGTCTGCGCAACAGCTGGGGCGCGCGGC 61
273 TGTCTTCCACGACATCCCATGTGTTAAGCTCTCCGACGCCAAGTCTCCCATATGCA 332
62 ACAAGCGCTCATTTGTTGCTGCACTAACAACATCTGGCGCGCTGGCGCGGGGGGC 121
333 ACTATATATCATAGTCGCGGCTATACAACTACAGGCAAGCTGAACATCGAGTGGAGA 392
122 CGAGAGATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 181
393 AGGACCATGCAATTAAGTACG--TTCAAGTGTGTTCAATTCATCTGCTCTGTATCA 449
182 TCGTGAAGACTTGTGCTGTGCTGCGCGCATCACAGCCACATGCGGTGCGACGCTGG 241
450 TCCATAGAAATATTGTTGCTTAACTATTGGAAACCAAGAACTTCCACCGGCCA 509
242 TCTACTATTGCTGCTGTAACATCAAGCTGAGTGAAGTCTGCTACAGGCGCGCGCTACT 301
510 TGTACTATTTCATAGGCAACCTAGCCCTCTGAGACTGTAGAGAGAGTGTACACAG 569
302 CCAAGCTGCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 361
570 CTAAAGCTGCTGCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 629
362 GGAAGGCTGCTGCTGCTGCAAGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCG 421
630 GGAAGGAGATATTGTTGAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 689
422 GGAAGGCTTGGCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 481
690 TTGAGCGCTATACACATGCTGAAGATGAAGATGAAGATGAAGATGAAGATGAAG 746
482 GCGCTACGCGCTTATCGGCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 541
747 GCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 806
542 TGTGGGCTGAAGTGGCTGTGCGCTTGTGACCGCTGCTGACCGCTTGTGCGCTCTACT 601
807 TCATGGGCTGGAACATGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 866
602 CCAAGGCTTACATCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 661

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RESULT 6
US-08-196-989B-3
; Sequence 3, Application US/08196989B
; Patent No. 5585476
; GENERAL INFORMATION:
; APPLICANT: MacLennan, A. John
; TITLE OF INVENTION: Molecular Cloning and Expression of
; TITLE OF INVENTION: G-Protein Coupled Receptors
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Saliwanichik & Saliwanichik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: US
; ZIP: 32606
; COMPUTER READABLE FORM:

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Db 867 ACAACACTATATCTCTGACACGCGCTTCACCCCTGCTTCATGCTCA 926
 QY 662 GCGCTATAGGGCCATCTTCCGCTGCTGACAGCGCCAGAGGCCCAAGGCC 721
 Db 927 TCCCTACTGAGGATCTACTCTGCTGAGGACGAGCGCGGCTGACCTTCCGA 986
 QY 722 CGGCGCGCGAGAGGCCCGCGG-----CCTGCTGAAGACGGTGC 760
 Db 987 AGAACATCTCCAGAGCGCGAGCGAGTTCGAGAAAGTCTGCGCTTGTGTAAGCA 1046
 QY 761 TGAATATCTCTGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 820
 Db 1047 TCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1106
 QY 821 AGCTCTTGGCTCCACCTCTGCGGCGCAGAGTACCTGCGGCGATGACTGAT 880
 Db 1107 ATG---TGGGATGCAAGGCGAGAACCTGTGACATCTCTTACAAAGAGAGT 1163
 QY 881 CCGTGGCGCTCTCACTGCGGCGGTACACCCATCATCTCTCTCCGACGAGGAG 940
 Db 1164 TTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1223
 QY 941 TGTGAGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 971
 Db 1224 TCGCGCGGCGCTTCAATCAGATCATATCTTG 1254

RESULT 7

US-08-760-936-3
 ; Sequence 3, Application US/08760936
 ; Patent No. 5856443
 ; GENERAL INFORMATION:
 ; APPLICANT: MacLennan, A. John
 ; TITLE OF INVENTION: Molecular Cloning and Expression of
 ; -TITLE OF INVENTION: G-Protein Coupled Receptors
 ; NUMBER OF SEQUENCES: 14
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
 ; STREET: 2421 N.W. 41st Street, Suite A-1
 ; CITY: Gainesville
 ; STATE: FL
 ; COUNTRY: US
 ; ZIP: 32606
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/760,936
 ; FILING DATE: December 6, 1996
 ; CLASSIFICATION: 536
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Pace, Doran R.
 ; REGISTRATION NUMBER: 38,261
 ; REFERENCE/DOCKET NUMBER: MAC-100C1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 352-375-8100
 ; TELEFAX: 352-372-5800
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2232 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 269..1420
 ; US-08-760-936-3

Query Match 19.9%; Score 230.2; DB 2; Length 2232;
 Best local, similarity 55.3%; Pred. No. 3,1e-35;

Matches 548; Conservative 0; Mismatches 413; Indels 30; Gaps 4;
 QY 2 TGAACGCCAGGGAGACCCGATGAGCCCGGAGTCTGCCAACAGCTGAGCGGCGGC 61
 Db 273 TGTCTCCACAGGATCCAGTGTAAAGCTCTCCGAGGCAAGTCTCCGATATGAGA 332
 QY 62 ACAGCGGCGCTATGTTCTGCACTACACCACTCGGCGGCGGCTGAGCGCGGCGGC 121
 Db 333 ACTATGATATATATAGTCCGGCATTACACTACAGAGGCACTGACATGAGATGAGA 392
 QY 122 CGAGAGATGCGGCGCTGAGGCGCTGCGGCGGCTGCGTGGTGGCGCCAGCTGCT 181
 Db 393 AGACCATATATATATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 449
 QY 182 TGTGAGAACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 241
 Db 450 TCTTGAATATATATATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 509
 QY 242 TCTATATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 301
 Db 510 TGTACTATTTATAGGCAACCTGACCTCTGAGACCTGTTAGCAGGAGTGGCTTAC 569
 QY 302 CCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 361
 Db 570 CTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 629
 QY 362 GGGAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 421
 Db 630 GGGAGGAGATATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 689
 QY 422 GGGAGCGCTTGGCCACCATGATGATGATGATGATGATGATGATGATGATGAT 481
 Db 690 TTGACGCTACATCATCATCATCATCATCATCATCATCATCATCATCATCAT 746
 QY 482 GCGTACGCGCTTATGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 541
 Db 747 GCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 806
 QY 542 TCGTGGGCTGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 601
 Db 807 TCAATGCTGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 866
 QY 602 CCAAGCGCTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 661
 Db 867 ACAACACTATATATCTCTGACACGCGCTTCACCCCTGCTTCATGCTCA 926
 QY 662 GCGCTATAGGGCCATCTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 721
 Db 927 TCCCTACTGAGGATCTACTCTGCTGAGGACGAGCGCGGCTGACCTTCCGA 986
 QY 722 CGGCGCGCGAGAGGCCCGCGG-----CCTGCTGAAGACGGTGC 760
 Db 987 AGAACATCTCCAGAGCGCGAGCGAGTTCGAGAAAGTCTGCGCTTGTGTAAGCA 1046
 QY 761 TGAATATCTCTGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 820
 Db 1047 TCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1106
 QY 821 AGCTCTTGGCTCCACCTCTGCGGCGCAGAGTACCTGCGGCGATGACTGAT 880
 Db 1107 ATG---TGGGATGCAAGGCGAGAACCTGTGACATCTCTTACAAAGAGAGT 1163
 QY 881 CCGTGGCGCTCTCACTGCGGCGGTACACCCATCATCTCTCTCCGACGAGGAG 940
 Db 1164 TTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1223
 QY 941 TGTGAGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 971
 Db 1224 TCGCGCGGCGCTTCAATCAGATCATATCTTG 1254

RESULT 8
 US-09-542-733-1

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; Sequence 1, Application us/09542733
; Patent No. 6323333
; GENERAL INFORMATION:
; APPLICANT: Ping Tsui
; TITLE OF INVENTION: Mouse EDG1
; FILE REFERENCE: GP-70610
; CURRENT APPLICATION NUMBER: US/09/542,733
; CURRENT FILING DATE: 2000-04-04
; EARLIER APPLICATION NUMBER: 60/127,696
; EARLIER FILING DATE: 1999-04-05
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1149
; TYPE: DNA
; ORGANISM: MUS MUSCULUS
US-09-542-733-1

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Query Match      19.2%; Score 221.6; DB 4; Length 1149;
Best Local Similarity 54.7%; Pred. No. 1,2e-33;
Matches 543; Conservative 0; Mismatches 419; Indels 30; Gaps 4;

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OY 1 ATGAAGCCACGAGGAGCCCGGCTGGCCCGGAGTCCGACAGCTGGGGGCGGCGG 60
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 ATGGTCCCACTAGCATGATCCCGAGGTAAAGCTCTCCGACACTGATCTGACATGG 60
OY 61 CACAGCCGCGCTATGTTGCTGACATACAGCACTCGGGCGCGCTGGCGGCGGG 120
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 AACTATGATATCATAGTCCGCAATTAACAACAGAGCAAGTTGAAC---ATCGGGGCG 117
OY 121 CCGGAGGATGGGCGCTGGGGGCGCTGGGGGCGCTGGGGGCGGCGGCTGGTG 180
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 118 GAGAGGACCATGCGCTTAACTGACTTCAGTGGTTCATTCATCTGCTGCTTATC 177
OY 181 GTGCTGAGAACTTGTGTGTGTGGCGGCAATCACACCATGCGGTGCGAGCTGG 240
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 178 ATCCTAGAGAAATATATTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 237
OY 241 GTCTACTATTGCTGGTGGTACATCAGCTGAGTGCCTGCTCAGGGGCGGCGTACTG 300
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db - 238 ATGCTACTATTCTATGAGCACTAGCCCTCTGCGACTTATTGAGAGGCTGGCTTAC 297
OY 301 GCCAACGTGCTGCTGGGGGCGGCGACCTTCCGCTGGGCGCGCCGCGGCTTCT 360
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 298 GCTAACCTGCTGTGTCTGGGGCGGCGACCACTTACAGCTCACACCTGCCAGTGTCTG 357
OY 361 CCGGAGGCGCTGCTCTTACCGCGCGGCGGCGCTTCCAGCTTCCAGCTTCTTAC 420
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 358 CCGGAGGAGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 417
OY 421 GGGGAGCGCTTGGCCACATGAGTGGCGGCGGTGGCCGAGAGCGGGCCACCAAGCAGC 480
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 418 ATTGAGCGCTACATCACCTGTCTGAAAGTGAACACTACACAGCGG---AGCAAGAGTGC 474
OY 481 CGGCTTACAGGCTTATCGGCGCTTGGCGGCTGCTGGCGGCGGCGGCGGCGGCGCT 540
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 475 CGCTCTTCTGTGTATCAGCGCGCTGCTGGGCTATCTTCCATCTTGGGGGCGCTGCCC 534
OY 541 TTGCTGGGCTGAAGTGCCTGTCGCTTTTGAACGCTGCTCCAGCTTCTTGGCCCTTAC 600
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 535 ATCATGGGCTGAGAACTGATCAGCTGCTGCTTACGCTCTCCACCGTGTCTCCCTTAC 594
OY 601 TCCAGGCGCTACCTCTCTTGGCGGCTTGGCGGCGGCGGCGGCGGCGGCGGCGGCG 660
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 595 CACAGACACTATTTCTCTTCTGACACACCGCTTTCATCTGCTGCTTCTTCTTCTGCTG 654
OY 661 GGCCTCTATGAGGCGCATCTTCCGCTGTGTCAGGCGGCGGCGGCGGCGGCGGCGGCG 720
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 655 ATCTCTACTGCGAGATCTACTCTTGTGTCAGAGACTCGAAGCCCGCGCTGACTTCCGC 714
OY 721 GCGGCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 759
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 715 AAGAACATCTCCAGGCGCGAGTCTGTGAGAGTCTTGTGCGCTTGTCTGTAAGAGGCTG 774

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OY 760 CTGATGATCTGCTGCGCTTCTGCTGCTGGGGCGGCGGCGGCGGCGGCTGCTGCGC 819
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 775 ATCATGCTCTGAGTGTCTTATGCTGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGG 834
OY 820 GACGCTTTTGGCTTCCAACTGCTGGGCGGCGGAGTACCTGCGGGCGGAGTGGATCTG 879
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 835 GATG---TGGGCTGCAAGGCGGAGACCTGTGACATCTGTACAAAGAGAGTACTTCTG 891
OY 880 GCCCTGGCGCTCTCAACTGCGGCTGCAACCCCATCATCTACTCTTCCGAGAGGAG 939
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 892 GTTCTGCTGTGTGAGCTGACCTGATACCAACCCCATCATCTACTCTTCCGAGAGAG 951
OY 940 GTGTGAGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 971
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Db 952 ATGCGCGGCGGCTTTCATCCGATCTGATCTTG 983

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RESULT 9
US-08-789-982-1
; Sequence 1, Application us/08789982
; Patent No. 6037146

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; GENERAL INFORMATION:
; APPLICANT: Sathe, Ganesh
; TITLE OF INVENTION: CDNA CLONE HBCH90 THAT ENCODES
; TITLE OF INVENTION: A NOVEL 7- TRANSMEMBRANE RECEPTOR
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/789,982
; FILING DATE: 28-JAN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Han, William T
; REGISTRATION NUMBER: 34,344
; REFERENCE/DOCKET NUMBER: ATG50050
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5219
; TELEFAX: 610-270-4026
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1260 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-789-982-1

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Query Match      15.8%; Score 182; DB 3; Length 1260;
Best Local Similarity 53.8%; Pred. No. 3.3e-26;
Matches 477; Conservative 0; Mismatches 385; Indels 24; Gaps 4;

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OY 139 GGGGCGCTGCGGGGCGTGTGCTGCGCGGCGGCGGCTGCTGCTGCTGCTGCTGCTG 198
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 229 GTGCTCGTGTGCGACCTGAGGCGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTG 288
OY 199 GTGCTGGGCGGCTATCACAGCACTGCGGCTGCGGCGGCGGCTGCTGCTGCTGCTG 258

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Db 289 GTCATACAGCATCGCTCCAAACCGCGCTTCACACAGCCCATCTACTACCTGGCGGC 348
QY 259 AACATCAGCGTGAAGTACCGCTGCACAGGGGCGCGCTTACTGGCCACAGCTGCTGTCG 318
Db 349 AATGTGCGCGGGGTGACCTCTTGGGGGCTGCTTACTCTTCTCTCATGTCACACT 408
QY 319 GGGGCGCGACCTTCGCTGAGGCGCGCCACAGTGGTCTTACAGGGAGCGCTGCTCTTC 378
Db 409 GGTCCCGCGACAGCCGACTTTCATTGAGGGGTGTGTCTCGCGAGGCTTGTGAGAC 468
QY 379 ACCGCGCTGGCGCGCTTCCACTTACAGCTGCTTCTTACTGCAAGGGAGCGCTTGGCAC 438
Db 469 ACAAGCTTCACTGCTGTGGTGGCGACACTGCGCATGCGGTGAGAGCG---GCACCGC 525
QY 439 ATGTGCGCGCGGTGCGCGACAGACGGCGCACACACACAGCGCGGTCTAGGCGCTCATC 498
Db 526 AGGTGATGCGCGGTGACAGCTGCACACCGCGCTGCGCGCGGTGCTCATGCTCAT 585
QY 499 GGGCTCTGCTGCTGCTGCGCGCGCTGCTGAGGAGTGCCTTGTGCTGAGCAACTGC 558
Db 586 GTGGGCGTGTGGTGGCTGCGCGCGCTGCGCGCGCTGCTGCGCGCGCTGCGCGCTG 645
QY 559 CTGTGCGCGCTTACCGCTGCTGCTGCTTTCGCGCGCTGCTGCGCGCGCTGCTGCTG 618
Db 646 CTGTGCGCGCTTACCGCTGCTGCTGCTTTCGCGCGCTGCTGCGCGCGCTGCTGCTG 705
QY 619 TTCT-----GCTGTGATCTTTCGCGCGCGCTGCTGCGCGCGCTGCTGCTGCTG 666
Db 706 GTCTGCGCGCTTTCGAGCGCTGCTGCTTCTGCTCATGAGTGGTGTACACCGCGCAT 765
QY 667 TATGGGCGCATCTTCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 726
Db 766 TTCTTTTACGTGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 825
QY 727 CGCGCGAGAGCG---CGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 783
Db 826 TACCGAGAGACACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 885
QY 784 GTGTGCTGGGGGCGCACTCTTCCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 843
Db 886 GTGTGCTGAGACACAGCGCGAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 939
QY 844 GCCCAGAGTACTGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 903
Db 940 TCTGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 999
QY 904 GTCAACCCCATATCTACTCTTCCGAGACAGGAGGTGTGCTGCTGCTGCTGCTGCTGCTG 963
Db 1000 GTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1059
QY 964 CTGTGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1009
Db 1060 CTGTGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1105

```

RESULT 10
US-08-861-747-1
Sequence 1, Application us/08861747
Patent No. 6020158

GENERAL INFORMATION:
APPLICANT: MONROE, Donald G.
APPLICANT: VYAS, Tejal B.
TITLE OF INVENTION: A HUMAN EDG-6 RECEPTOR HOMOLOG
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nikaido, Marmelstein, Murray & Oram LLP
STREET: 655 15th St., NW, Suite 330 - G Street Lobby
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-5701
COMPUTER READABLE FORM:

```

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/861,747
FILING DATE: 22-MAY-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Jahns, Kristina M.
REGISTRATION NUMBER: 41,092
REFERENCE/DOCKET NUMBER: P8074-7003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 638-5000
TELEFAX: (202) 638-4010
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1761 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-861-747-1

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Query Match 15.5%; Score 178.8; DB 3; Length 1761;
Best Local Similarity 53.6%; Pred. No. 1.4e-25;
Matches 475; Conservative 0; Mismatches 387; Indels 24; Gaps 4;

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QY 139 GGGGCGCTCGGGGGCTGCTGCTGCGCGCGCACTGCTGCTGCTGCTGCTGCTGCTG 198
Db 187 GTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 246
QY 199 GTGTGCGCGCATCACCAGCCACATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 258
Db 247 GTATATGAGCGCATGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 306
QY 259 AACATCAGCTAGTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 318
Db 307 AATCTGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 366
QY 319 GGGGCGCGCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 378
Db 367 GGTCCCGCACAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 426
QY 379 ACCGCGCTGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 438
Db 427 ACAAGCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 483
QY 439 ATGTGCGCGCGGTGCGCGAGAGGGGGCGCACAGACACAGCGCGCTGCTGCTGCTGCTGCTG 498
Db 484 AGTGTGATGCGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 543
QY 499 GGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 558
Db 544 GTGGGCGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 603
QY 559 CTGTGCGCGCTTGAACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 618
Db 604 CTGTGCGCGCTGAGCGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 663
QY 619 TTCT-----GCTGTGATCTTTCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 666
Db 664 GTGTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 723
QY 667 TATGGGCGCATCTTCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 726
Db 724 TTTTATATGCTGCGCGCGCGCGAGTGCATGCGAGATGTACAGTGTGCTGCTGCTGCTGCTGCTG 783
QY 727 CGCGCGAAGCG---CGCGCGCTGCTGAGAGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 783
Db 784 TACCGAGAGACACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 843
QY 784 GTGTGCGCGCGCGCATCTTTCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 843

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QY 530 GGATGCTCTTGTGGGCTGAAGTCCCTGCGCTTTGACCGCTGCTCCAGCTTC 589
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 635 GTGGCTTCCCATCTCTGGGCTGGAAATGTCGACATCTGGAGGCTTGGCTCCACTGTGC 694
QY 590 TGCCCTCTACTCCAGGCGTACATCCCTTCTGCTGATGATCTTGGCGGCGCTCTGG 649
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 695 TGCCCTCTACTAGACACTATGCTGCTGCGGTGACACATCTCTCTGATCTTAC 754
QY 650 CCACATCATGAGGCTCTATGAGGCGCATCTTCCGCTGTGACAGGCCAGGCGAGAAG 709
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 755 TGGTATCTGAGGCTTGTAGCTCCGAATCTACTGTAGTCCGCTCAAGCATGAGGAGC 814
QY 710 CCCCAGCCGAGCGCGCGCGCGCGCGCTGCTGAGAGCGGTCTGATATCC 769
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 815 TTGCTGTCTC-----AGACGCTGGCGCTGTCAAGACAGTACCATCTGAC 862
QY 770 TGTGGCTTCTGCTGCTGCTGAGGCGCGCTTCTGCGGCTGTGCTGCGGAGCTTTG 829
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 863 TGGGTGTTTTCATCTGCTGCTGGCTGGCTTTTACATCTCTCTTGA---CTCTA 919
QY 830 GCTCCACCTTGGGCGGAGAGTACTGCGGCGCATGAGTGAATCTTGGCTGCGCG 889
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 920 CCTGTCCGTCGCGGCTGTCTGTCTACAAAGCCCATTTATTTTGTCTGCGCA 979
QY 890 TCTCACTGCGGCTCAACCCCATCTACTCTTCCGAGAGGAGAGGTGTGAGAG 949
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 980 CCGTCACTCTCTGCTCAACCTCTCTATCTATCATGCGCTACCGGAGCTTGGAGGG 1039
QY 950 CCGTCTCACTCTCTGCTGCTGCGGCTGTCTCGGCTGAGGAGGCGCGGG 1006
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1040 AGGACTGAGGCGGCTGCTGTGCTGGCGGAGGAGGAGGAGGAGGAGGAGGAG 1096

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RESULT 14
US-08-763-938-1
; Sequence 1, Application US/08763938
; Patent No. 6140060
; GENERAL INFORMATION:
; APPLICANT: CHUN, Jerold J.M.
; APPLICANT: HECHT, Jonathan H.
; TITLE OF INVENTION: CLONED LYSOPHOSPHATIDIC ACID
; TITLE OF INVENTION: RECEPTORS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nikaido, Maimelstein, Murray and Oram LLP
; STREET: 655 15th Street, N.W., Suite 330 - G St. Lobby
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-5701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/763,938
; FILING DATE: 12-Dec-1996
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: JAHNS, Kristina M.
; REGISTRATION NUMBER: 41,092
; REFERENCE/DOCKET NUMBER: P8074-6018
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 638-5000
; TELEFAX: (202) 638-4810
; INFORMATION FOR SEQ ID NO: 1:
; LENGTH: 2250 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

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MOLECULE TYPE: CDNA
US-08-763-938-1

Query Match 11.2%; Score 129.4; DB 3; Length 2250;
Best Local Similarity 50.1%; Pred. No. 2.7e-16;
Matches 424; Conservative 0; Mismatches 396; Indels 27; Gaps 3;

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QY 146 TGGCGGGGCTGTGCGGCGCGCGCGCTGCTGAGTGTGCTGAGAACTTGTGCTGG 205
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 382 TGATGGAGCTGGGCGATCACTGTTTGGCTGTTCATATGTTGGCAATCTCTGGTCAATG 441
QY 206 CGGCGCATCAACACCCAGCCAGTCCGCGAGCTGAGTCTACTATTGCTGTGAACATCA 265
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 442 TGGCAATCTACGTCACCCCGCTTCATTTCTTATTTATTTACTTGTGATGCAACTGG 501
QY 266 CGCTGAGTACCTGCTCAAGCGCGCGCGCTTACTGCGCAAGCTGTCTGTCGCGGGGCC 325
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 502 CTGCTGCAACTTCTTTCGCTGATTTGGCTTACTTCTACTGATGTTCAATACAGGACTGA 561
QY 326 GCACCTTCCGTGTGGCGCGCGCGCGAGTGTCTACGAGGAGGCGCTGCTTCAACCGCC 385
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 562 ATACCGGAGACTGACTGTTTACAGGTGCTCTCGGAGGCGCTTATGACACAGACC 621
QY 386 TGGCGCGCTCCACCTTCAACCTGCTCTTACTGCAAGGAGCGCTTTCACCATGCTGC 445
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 622 TACACATCTTGTGGCGCAACCGCTGTGCTATTGCTATGAGAGGCACATCAAGCTTTTC 681
QY 446 GCGCGGTGCGGAGAGCGGCGCGCGCGCACCAAGACCGCGGTACGGCTTCAATCGGCTCT 505
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 682 GCATGAGCTCCATACAGATGAGCAA---CGGCGGCTGTGTGTGATGATGATCA 738
QY 506 GCTGCTGCTGCGCGCGCTGCTGAGGAGTGTGCTGCTGAGGAGTGTGCTGAGTGTGCTG 565
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 739 TCTGACTATGSCCAATTGATGATGCTGTATACCAAGTGTGAGGAGGAGGAGGAGTGTG 798
QY 566 CTTTGAACCGCTGCTGCAACCTTGTGCGCTTCTACTCAAGCGCTCAATCTTCTGCTG 625
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 799 AATGATGATCTGTTTCAACATGAGGCGCGCTTCAAGTACTTACTTGTCTGCTG 858
QY 626 TGTGATCTTCCGCGCGCTGCTGCGCGCATATGAGGCGCTTATGAGGCGCATCTTCCGCC 685
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 859 CCATTTTCACTGCTGAGCTTTTGTGCTATGATGATGCTTCTGAGCTCAATCTTGTGCT 918
QY 686 TGTCTCAGGCGAG-----CGGCGAGAGGCGCGCGCGCGCGCGCGCGCGCGCGCG 730
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Db 919 ATGTTGCGCAGAGGACTATGAGGATGCTCGGCAATGTTGAGAACCGAGAGGAGATGGG 978
QY 731 GCAAGCGCGCGCGCTGCTGAGAGGAGGCTGATGATCTGCTGCTGCTGCTGCTGCT 790
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Db 979 ACACCATATAGAGCGCTTGTGAAGACTGTGTCATTTGTGCTGCTGCTTATTTGTGCT 1038
QY 791 GGGGCCCACTTTCGGGCTGCTGCGCGAGCGCTTGTGCTCAACCTCGGGGCCAGG 850
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Db 1039 GGACTCCGGGATGTGCTTTGATTTGATGATGATGCTGCGCGAGTGCATGCTGCTGG 1098
QY 851 AGTACTCGGCGGAGTGAAGTCTGAGGCGCTGCGCGCTGCAACTCGGCGGCTCAAC 910
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Db 1099 CCTA-----TGAGAAATTTCTTCTCTCTGCGCGAGATTCACATCTGCTATGACC 1149
QY 911 CCATCATCTACTCTTCCGAGAGGAGGAGTGTGACAGCGCTCTAGCTTCTGCTGCT 970
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Db 1150 CCATCATCTACTCTTCCGAGAGGAGGAGTGTGACAGCGCGCTCTAGCTTCTGCTGCT 1209
QY 971 GCGGCTG 977
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Db 1210 GCGAGCG 1216

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RESULT 15
US-08-467-948A-3
; Sequence 3, Application US/08467948A
; Patent No. 5998164
; GENERAL INFORMATION:

```

APPLICANT: LI, YI
 APPLICANT: CAO, LIANG
 APPLICANT: NI, JIAN
 APPLICANT: GENTZ, REINER
 APPLICANT: BULT, CAROL J.
 APPLICANT: SUTTON III, GRANGER G.
 APPLICANT: ROSEN, CRAIG A.
 TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein
 TITLE OF INVENTION: Coupled Receptor GPR2
 NUMBER OF SEQUENCES: 30
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
 STREET: 1100 NEW YORK AVE., NW, SUITE 600
 CITY: WASHINGTON
 STATE: DC
 COUNTRY: USA
 ZIP: 20005
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY DISK
 COMPUTER: IBM PC COMPATIBLE
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/467,948A
 FILING DATE: 06-JUN-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/04079
 FILING DATE: 30-MAR-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: STEFFE, ERIC K.
 REGISTRATION NUMBER: 36,688
 REFERENCE/DOCKET NUMBER: 1488.1140003/EKS/KLM
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-371-2600
 TELEFAX: 202-371-2540
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2185 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: both
 TOPOLOGY: both
 MOLECULE TYPE: CDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 884..2062
 US-08-467-948A-3

Query Match 9.9%; Score 114; DB 2; Length 2185;

Best Local Similarity 51.9%; Pred. No. 2,1e-13;

Matches 416; Conservative 0; Mismatches 360; Indels 26; Gaps 6;

QY 224 TCGGTCGCGAGCGTGGCTACTATGTCGCTGTAACATCAGCGTGAAGTGAACCTGCTCA 283
 DB 1072 TACGCTGTGCGAGTGAAGTACTCTCCGCCCAATCTGTCCGGCGCTGAACCTCTTGC 1131
 QY 284 CGGCGCGCGCTACCTGGCCCAACGTGCTGTCTCGGGGAGCCGCACTTCGCTGCGC 343
 DB 1132 CGGGGTGGCTACTCTTCCATGTTCCAAAC-TGTCCCGGACAGCCGACTTTCAC 1190
 QY 344 CCGCCAGTGTCTTCTACGAGGAGGCGCTGCTTTCACCGCCCTGGCGCTTCACCTTCA 403
 DB 1191 TTGAGGGCTGTCTCTGCGAGGGCTGTGACACAAACTCTCACTGCTGTGGGCCA 1250
 QY 404 GCCTGTCTTCACTGAGGGAGAGCGCTTGGCCACATGATGGCGGCGGCGAGAGCG 463
 DB 1251 CACTGTGTGGCATGCGCGTGGAGCGCACCGCATGTGTATGGCGCTGCACGCTGCACAGCC 1310
 QY 464 GGGCCACCAAGACAGCCGCTCTACGAGCTTCATGCGCTTGTGCTGTGCTGCGCGCGC 523
 DB 1311 GCTGTGCGCGT---GCGCGTGTCTATGTGTGGCGTGTGGGTGGCTGCCCTGG 1367
 QY 524 TGTGTGGGATGTGCTTTGTGTGGGCTGGAAGTGCCTGTGCGCTTTGACCGCTGTCTCA 583

DB 1368 GCTTGGGCTGTGCTGCTGCGCCACTGTGGCACTGCTCTGTGTCCTGAGACCGCTCTTAC 1427
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 DB 1428 GCATGACACCCCTGCTCAACCGCTCTCTATTTGGCGTGGGCTGTGCAAGCTGCTTG 1487
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Search completed: December 13, 2002, 10:15:57
Job time : 86 secs